



A13

SEQUENCE LISTING

<110> Peter
Garman, Jonathan David
Candia III, Albert Frederick
Arbor Vita Corporation

<120> CLASP-3 Transmembrane Protein

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<140> US 09/737,246

<141> 2000-12-13

<150> US 60/160,860

<151> 1999-10-21

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<170> PatentIn Ver. 2.1

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aca aca ttt cct gat cag gtc cag gat ctg gtt ttc aat ctc cat atg Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His Met 1630 1635 1640	4947
att ctt tct gat act gtg aaa atg aag gaa cac cag gag gat cct gaa Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu 1645 1650 1655	4995
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Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg	
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Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys	
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Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu	
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Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg	
1915 1920 1925 1930	
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Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His Gly Glu	
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Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser His Ala	
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Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu Glu Ile	
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Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys Lys Thr	
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Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro Lys Met	
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Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln Gly	
2015 2020 2025	
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Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp Pro	
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Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe	
2045 2050 2055	
act aaa agg tgt gaa gat gcc tta aga aaa aat aag agc tta att ggg	6243
Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly	
2060 2065 2070	
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Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro	
2075 2080 2085 2090	

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Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
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Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
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Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
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Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
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Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
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Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
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cac	tat	gtt	aca	tta	aac	tta	ccc	tgc	agc	tta	ctt	act	cca	cct	gca	769
His	Tyr	Val	Thr	Leu	Asn	Leu	Pro	Cys	Ser	Leu	Leu	Thr	Pro	Pro	Ala	
				245					250					255		
tct	cca	tca	cct	tct	gtt	tct	tct	gca	aca	tct	cag	agt	tct	gga	ttt	817
Ser	Pro	Ser	Pro	Ser	Val	Ser	Ser	Ala	Thr	Ser	Gln	Ser	Ser	Gly	Phe	
			260					265					270			
tct	acg	aat	gta	caa	gac	caa	aag	att	gca	aat	atg	ttt	gaa	tta	tcc	865
Ser	Thr	Asn	Val	Gln	Asp	Gln	Lys	Ile	Ala	Asn	Met	Phe	Glu	Leu	Ser	
		275					280					285				
gtg	cct	ttc	cgc	caa	cag	cat	tat	ttg	gca	gga	ctt	gtg	tta	aca	gag	913
Val	Pro	Phe	Arg	Gln	Gln	His	Tyr	Leu	Ala	Gly	Leu	Val	Leu	Thr	Glu	
	290					295					300					
ctg	gct	gtc	att	tta	gac	cct	gat	gct	gaa	gga	ctg	ttt	gga	ttg	cat	961
Leu	Ala	Val	Ile	Leu	Asp	Pro	Asp	Ala	Glu	Gly	Leu	Phe	Gly	Leu	His	
305					310					315					320	
aag	aaa	gtc	atc	aat	atg	gta	cac	aat	tta	ctc	tcc	agt	cac	gac	tca	1009
Lys	Lys	Val	Ile	Asn	Met	Val	His	Asn	Leu	Leu	Ser	Ser	His	Asp	Ser	
				325					330					335		

gac	ccg	cgg	tac	tct	gac	cct	cag	ata	aag	gct	cga	gtg	gcc	atg	ttg	1057
Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala	Met	Leu	
			340					345					350			
tat	cta	cct	ctg	att	ggc	att	atc	atg	gaa	act	gta	cct	cag	ctg	tat	1105
Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln	Leu	Tyr	
			355				360					365				
gat	ttt	aca	gaa	act	cac	aat	caa	cga	gga	aga	cca	att	tgt	ata	gcc	1153
Asp	Phe	Thr	Glu	Thr	His	Asn	Gln	Arg	Gly	Arg	Pro	Ile	Cys	Ile	Ala	
	370					375					380					
act	gat	gat	tat	gaa	agt	gag	agc	gga	agt	atg	ata	agc	cag	acc	gtt	1201
Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln	Thr	Val	
385					390					395					400	
gcc	atg	gca	atc	gca	ggg	aca	tcg	gtc	cct	caa	cta	aca	agg	cct	ggc	1249
Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg	Pro	Gly	
				405					410					415		
agt	ttc	ctc	ctc	acg	tca	acg	agt	ggc	agg	caa	cac	act	acc	ttt	tca	1297
Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr	Phe	Ser	
			420					425					430			
gca	gaa	tca	agt	cga	agc	ctt	ttg	atc	tgt	cta	ctt	tgg	gtt	ctc	aaa	1345
Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val	Leu	Lys	
		435					440					445				
aat	gca	gat	gaa	aca	gtt	cta	cag	aag	tgg	ttt	aca	gat	ctc	tca	gtc	1393
Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu	Ser	Val	
	450					455					460					
ttg	cag	cta	aac	cgg	cta	tta	gat	ctg	ctt	tat	ctc	tgt	gtg	tct	tgc	1441
Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val	Ser	Cys	
465					470					475					480	
ttt	gag	tat	aaa	ggg	aaa	aaa	gtg	ttt	gaa	cga	atg	aat	agc	ttg	acc	1489
Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser	Leu	Thr	
			485					490					495			
ttt	aag	aaa	tca	aaa	gac	atg	aga	gca	aag	ctt	gaa	gaa	gct	att	ctt	1537
Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala	Ile	Leu	
			500					505					510			
ggg	agc	ata	ggc	agg	caa	gaa	atg	gta	cgg	cga	agc	cga	gga	cag		1585
Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg	Gly	Gln	
		515					520					525				
ctc	gag	aga	agc	cca	tct	gga	agt	gcc	ttt	gga	agt	caa	gaa	aat	ttg	1633
Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu	Asn	Leu	
		530				535					540					
agg	tgg	agg	aaa	gat	atg	act	cac	tgg	cgt	caa	aac	aca	gag	aag	ctt	1681
Arg	Trp	Arg	Lys	Asp	Met	Thr	His	Trp	Arg	Gln	Asn	Thr	Glu	Lys	Leu	
545					550					555					560	
gac	aaa	tca	aga	gca	gag	att	gaa	cac	gaa	gca	ctg	att	gat	gga	aac	1729
Asp	Lys	Ser	Arg	Ala	Glu	Ile	Glu	His	Glu	Ala	Leu	Ile	Asp	Gly	Asn	
				565					570					575		

ctg gct aca gaa gca aac cta atc att tta gat aca tta gag att gtt Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu Ile Val 580 585 590	1777
gtt cag acc gtt tct gta acg gaa tcc aaa gag agc att ctt ggt gga Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu Gly Gly 595 600 605	1825
gtg cta aaa gtg cta cta cac agc atg gcc tgt aac caa agt gca gtt Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser Ala Val 610 615 620	1873
tat cta caa cac tgt ttt gct aca cag aga gcc ttg gtt tca aag ttt Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser Lys Phe 625 630 635 640	1921
cct gaa ctc tta ttt gaa gaa gag aca gag cag tgt gct gat tta tgc Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp Leu Cys 645 650 655	1969
ctc agg ctt ctc cga cac tgt agc agt agc atc ggt aca ata cgg tca Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile Arg Ser 660 665 670	2017
cac ccc agt gcc tcc ctt tac cta cta atg agg caa aac ttt gag att His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile 675 680 685	2065
ggg aat aac ttt gcc agg gtt aaa atg cag gta cca atg tca cta tcc Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser 690 695 700	2113
tcc ttg gtg ggc aca tct cag aat ttt aat gaa gaa ttc tta aga cgt Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg 705 710 715 720	2161
tct cta aag act ata ttg aca tat gct gaa gaa gat ctg gaa ttg agg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg 725 730 735	2209
gaa aca aca ttt cct gat cag gtc cag gat ctg gtt ttc aat ctc cat Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His 740 745 750	2257
atg att ctt tct gat act gtg aaa atg aag gaa cac cag gag gat cct Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro 755 760 765	2305
gaa atg ttg att gat cta atg tac aga att gcc aag ggt tac cag acc Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr 770 775 780	2353
tct cca gat ctg cga ttg acc tgg ttg cag aac atg gca ggc aag cac Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His 785 790 795 800	2401
tca gaa cga agc aat cat gct gaa gct gca cag tgt cta gtc cac tca Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser 805 810 815	2449

gca gca ctt gtt gct gaa tat ttg agc atg ctg gag gac cgg aaa tat	2497
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr	
820 825 830	
ctt cct gtg gga tgt gta aca ttt cag aat att tca tct aat gtt tta	2545
Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu	
835 840 845	
gaa gaa tct gcg gtc tca gat gat gtg gta tct cca gat gaa gaa ggt	2593
Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly	
850 855 860	
atc tgc tct gga aaa tac ttt act gag tca gga ctt gtg gga tta ctg	2641
Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu	
865 870 875 880	
gaa caa gca gct gct tcc ttc tct atg gct ggc atg tat gaa gca gtt	2689
Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val	
885 890 895	
aat gaa gtt tac aaa gta ctt att cct att cat gaa gct aat cgg gat	2737
Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp	
900 905 910	
gca aag aaa cta tcc aca att cat ggt aaa ctt caa gaa gca ttc agc	2785
Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser	
915 920 925	
aaa att gtt cat cag agt act ggc tgg gag cgg atg ttt ggc acc tat	2833
Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr	
930 935 940	
ttt cgt gtt ggt ttt tat gga acc aag ttc ggg gat ttg gat gaa caa	2881
Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln	
945 950 955 960	
gaa ttt gtt tac aag gag cct gca ata acc aaa ctt gca gag ata tct	2929
Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser	
965 970 975	
cac aga ttg gag gga ttt tac gga gaa aga ttt gga gag gat gtg gtt	2977
His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val	
980 985 990	
gaa gta atc aaa gac tct aat cct gta gac aag tgt aaa tta gat cct	3025
Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro	
995 1000 1005	
aac aag gca tat att cag att acc tat gtg gag cca tac ttt gac aca	3073
Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr	
1010 1015 1020	
tat gag atg aag gac aga atc acc tat ttc gac aaa aat tac aat ctt	3121
Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu	
1025 1030 1035 1040	
cgt cga ttc atg tac tgt aca ccc ttt act tta gat ggc cgt gcc cat	3169
Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His	
1045 1050 1055	

ggg gaa ctt cat gaa caa ttc aaa agg aag acc att ctg act acg tct 3217
 Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser
 1060 1065 1070

cat gcc ttt cct tat att aaa aca agg gtc aat gtc act cat aaa gaa 3265
 His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu
 1075 1080 1085

gag atc atc tta aca cca att gaa gtt gct att gag gac atg cag aaa 3313
 Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys
 1090 1095 1100

aag aca cag gag ttg gca ttt gca aca cat cag gat ccc gca gac ccc 3361
 Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro
 1105 1110 1115 1120

aaa atg ctt cag atg gta ctc cag gga tct gta ggc acc aca gtg aat 3409
 Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn
 1125 1130 1135

cag ggg cct ttg gaa gtt gcc cag gtt ttt ctg tct gaa ata cct agt 3457
 Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser
 1140 1145 1150

gac cca aag ctc ttc aga cat cat aat aaa ctg cga ctc tgc ttt aaa 3505
 Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys
 1155 1160 1165

gat ttt act aaa agg tgt gaa gat gcc tta aga aaa aat aag agc tta 3553
 Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu
 1170 1175 1180

att ggg ccg gtt caa aag gag tat caa agg gaa ttg ggg aaa cta tct 3601
 Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser
 1185 1190 1195 1200

tcg cct taa agaggcccta cagccctaga tcacagaaag tccctcagtt 3650
 Ser Pro

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aacatcgagt gtgaaaagat ctattggaaa ccaacatgga atggaattct ggaaattatt 3830

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 <213> Homo sapiens
 <223> preliminary CLASP-3

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 Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly Pro Lys
 35 40 45
 Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser Thr Gln
 50 55 60
 Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu Thr Ser
 65 70 75 80
 Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys Leu Phe
 85 90 95
 His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser Val Arg
 100 105 110
 Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met Val Lys
 115 120 125
 Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala Pro Arg
 130 135 140
 Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala Leu Val
 145 150 155 160
 Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp Thr Glu
 165 170 175
 Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn Asp Leu
 180 185 190
 Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys Ser Cys
 195 200 205
 Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro Ser Val
 210 215 220
 Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser His Glu
 225 230 235 240
 His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro Pro Ala
 245 250 255
 Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser Gly Phe
 260 265 270
 Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu Leu Ser
 275 280 285

Val	Pro	Phe	Arg	Gln	Gln	His	Tyr	Leu	Ala	Gly	Leu	Val	Leu	Thr	Glu	
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Leu	Ala	Val	Ile	Leu	Asp	Pro	Asp	Ala	Glu	Gly	Leu	Phe	Gly	Leu	His	
305					310					315					320	
Lys	Lys	Val	Ile	Asn	Met	Val	His	Asn	Leu	Leu	Ser	Ser	His	Asp	Ser	
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Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala	Met	Leu	
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Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln	Leu	Tyr	
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	370					375					380					
Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln	Thr	Val	
385					390					395					400	
Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg	Pro	Gly	
				405					410					415		
Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr	Phe	Ser	
			420					425					430			
Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val	Leu	Lys	
		435				440						445				
Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu	Ser	Val	
	450					455					460					
Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val	Ser	Cys	
465				470						475					480	
Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser	Leu	Thr	
				485					490					495		
Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala	Ile	Leu	
			500					505					510			
Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg	Gly	Gln	
		515					520					525				
Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu	Asn	Leu	
	530					535					540					
Arg	Trp	Arg	Lys	Asp	Met	Thr	His	Trp	Arg	Gln	Asn	Thr	Glu	Lys	Leu	
545				550						555					560	
Asp	Lys	Ser	Arg	Ala	Glu	Ile	Glu	His	Glu	Ala	Leu	Ile	Asp	Gly	Asn	
				565					570					575		
Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu	Ile	Val	
			580					585					590			
Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu	Gly	Gly	
		595					600					605				

Val	Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser	Ala	Val	610	615	620	
Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	Lys	Phe	625	630	635	640
Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp	Leu	Cys	645	650	655	
Leu	Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile	Arg	Ser	660	665	670	
His	Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	Glu	Ile	675	680	685	
Gly	Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser	Leu	Ser	690	695	700	
Ser	Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu	Arg	Arg	705	710	715	720
Ser	Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu	Leu	Arg	725	730	735	
Glu	Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn	Leu	His	740	745	750	
Met	Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	Asp	Pro	755	760	765	
Glu	Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr	Gln	Thr	770	775	780	
Ser	Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	Lys	His	785	790	795	800
Ser	Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val	His	Ser	805	810	815	
Ala	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg	Lys	Tyr	820	825	830	
Leu	Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn	Val	Leu	835	840	845	
Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	Glu	Gly	850	855	860	
Ile	Cys	Ser	Gly	Lys	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	Leu	Leu	865	870	875	880
Glu	Gln	Ala	Ala	Ala	Ser	Phe	Ser	Met	Ala	Gly	Met	Tyr	Glu	Ala	Val	885	890	895	
Asn	Glu	Val	Tyr	Lys	Val	Leu	Ile	Pro	Ile	His	Glu	Ala	Asn	Arg	Asp	900	905	910	
Ala	Lys	Lys	Leu	Ser	Thr	Ile	His	Gly	Lys	Leu	Gln	Glu	Ala	Phe	Ser	915	920	925	

Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr
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 Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
 945 950 955 960
 Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser
 965 970 975
 His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val
 980 985 990
 Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro
 995 1000 1005
 Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr
 1010 1015 1020
 Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu
 1025 1030 1035 1040
 Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His
 1045 1050 1055
 Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser
 1060 1065 1070
 His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu
 1075 1080 1085
 Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys
 1090 1095 1100
 Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro
 1105 1110 1115 1120
 Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn
 1125 1130 1135
 Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser
 1140 1145 1150
 Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys
 1155 1160 1165
 Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu
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Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	
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Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	Leu	Leu	Thr	Phe	
			20					25					30			
Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	
		35					40					45				
Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	
	50					55					60					
Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	Val	Ser	Ala	Asn	
65					70					75					80	
Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	Met	Gly	Arg	His	
				85					90					95		
Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	Pro	Leu	Leu	Lys	
			100					105					110			
Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	Asp	Gln	His	Leu	
		115					120					125				
His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	Gly	Ala	Gln	Ala	
	130					135					140					
Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	His	Ala	Met	Glu	
145					150					155					160	
Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	Asn	Gln	Leu	Phe	
				165					170					175		
Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	Val	Asn	Val	Thr	
			180					185					190			
Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	Glu	Gly	Leu	Glu	
		195					200					205				
Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	Ala	Glu	Pro	Tyr	
	210					215					220					
Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	Thr	Lys	Ser	Met	
225					230					235					240	
Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	Ser	Asn	Lys	Leu	
				245					250					255		
Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	Lys	Ser	Met	Ala	
			260					265					270			
Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	
		275					280					285				
Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	
	290					295					300					
Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	
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Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	
				325					330					335		
Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	
			340					345					350			
Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	
		355					360					365				
Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	
	370					375					380					
Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	
385					390					395					400	
Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	
				405					410					415		
Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	
			420					425					430			
Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	
		435					440						445			
Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	
	450					455					460					
Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	
465					470					475					480	
Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	
				485					490					495		
Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro	
			500					505					510			
Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	
		515					520					525				
Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile	
	530					535					540					
Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	
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Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	Ser	Leu	
				565					570					575		
Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	Arg	Cys	
			580					585					590			
Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu	
		595					600					605				
Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn	
	610					615					620					
Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val	
625					630					635					640	

Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile	Ala	Arg	Asn	
				645					650					655		
Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser	Gln	Thr	Leu	
			660					665					670			
Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	
		675					680					685				
Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	
	690					695					700					
Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	
705					710					715					720	
Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	
				725					730					735		
Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	
			740					745					750			
Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	
		755					760					765				
Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	
	770					775					780					
Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	
785					790					795					800	
Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	
				805					810					815		
Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	
			820					825					830			
Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	
		835					840					845				
Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu	Thr	
	850					855					860					
Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp	
865					870					875					880	
Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu	Thr	
				885					890					895		
Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	
			900					905					910			
Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	
		915					920					925				
Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	
	930					935					940					
Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	
945					950					955					960	

Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly
 965 970 975
 Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile
 980 985 990
 Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His
 995 1000 1005
 Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly
 1010 1015 1020
 Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu
 1025 1030 1035 1040
 Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp
 1045 1050 1055
 Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu
 1060 1065 1070
 Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu
 1075 1080 1085
 Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu
 1090 1095 1100
 Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe
 1105 1110 1115 1120
 Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
 1125 1130 1135
 Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
 1140 1145 1150
 Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
 1155 1160 1165
 Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
 1170 1175 1180
 Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
 1185 1190 1195 1200
 Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
 1205 1210 1215
 Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
 1220 1225 1230
 Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
 1235 1240 1245
 Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
 1250 1255 1260
 Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
 1265 1270 1275 1280

Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
1285 1290 1295

Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
1300 1305 1310

Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
1315 1320 1325

Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
1330 1335 1340

Met Thr Ser Ser Ser Ser Val Val
1345 1350

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Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
20 25 30

Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
35 40 45

Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
50 55 60

Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65 70 75 80

Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
85 90 95

His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
100 105 110

Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
115 120 125

Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
130 135 140

Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145 150 155 160

Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
165 170 175

Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
180 185 190

Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
 835 840 845
 Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
 850 855 860
 Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
 865 870 875 880
 Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
 885 890 895
 Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
 900 905 910
 Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
 915 920 925
 Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
 930 935 940
 Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
 945 950 955 960
 Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
 965 970 975
 Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
 980 985 990
 Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
 995 1000 1005
 Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
 1010 1015 1020
 Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
 1025 1030 1035 1040
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
 1045 1050 1055
 Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 1060 1065 1070
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
 1075 1080 1085
 Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
 1090 1095 1100
 His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
 1105 1110 1115 1120
 Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
 1125 1130 1135
 Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
 1140 1145 1150

Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
 1155 1160 1165
 Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
 1170 1175 1180
 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
 1185 1190 1195 1200
 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
 1205 1210 1215
 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1220 1225 1230
 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
 1235 1240 1245
 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
 1250 1255 1260
 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 1265 1270 1275 1280
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 1285 1290 1295
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 1300 1305 1310
 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
 1315 1320 1325
 Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 1330 1335 1340
 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
 1345 1350 1355 1360
 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 1365 1370 1375
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 1380 1385 1390
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 1395 1400 1405
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 1410 1415 1420
 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 1425 1430 1435 1440
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 1445 1450 1455
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 1460 1465 1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
1475 1480 1485

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
1490 1495 1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505 1510 1515 1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
1525 1530

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<213> Rattus norvegicus

<220>
<223> rat TRG

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Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
20 25 30
Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
35 40 45
Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
50 55 60
Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
65 70 75 80
Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
85 90 95
Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
100 105 110
Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
115 120 125
Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
130 135 140
Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
145 150 155 160
Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
165 170 175
Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
180 185 190
Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
195 200 205

Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	His	Val	Thr	Ala	
210						215					220					
Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Glu	Ala	Asp	Leu	Ala	Leu	Gln	
225					230					235					240	
Arg	Glu	Pro	Pro	Val	Phe	Pro	Tyr	Ser	His	Thr	Ser	Cys	Gln	Arg	Lys	
				245					250					255		
Ser	Arg	Gly	Gly	Met	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	
			260					265					270			
Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	
		275					280					285				
Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	
	290					295					300					
Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Leu	Arg	Ala	Gly	Leu	Leu	
305					310					315					320	
Thr	Ser	Ile	Asn	Ser	Ser	Ser	Pro	Ser	Met	Lys	Ser	Gly	Gly	Thr	Leu	
			325						330					335		
Glu	Thr	Thr	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Pro	Tyr	Ser	Lys	Val	
			340					345					350			
Thr	Glu	Val	Ile	Thr	Arg	Ala	Ala	Gly	Ser	Trp	Asp	Leu	Leu	Pro	Gly	
		355					360					365				
Gly	Leu	Phe	Gly	Gln	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr	
	370					375					380					
Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg	
385					390					395					400	
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met	
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Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Phe	
			420					425					430			
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Thr	Pro	Phe	Phe	Asp	Glu	Lys	Glu	
		435					440					445				
Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Cys	His	Asn	Ile	Arg	Arg	
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Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly	
465					470					475					480	
Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys	
			485						490					495		
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr	
			500					505					510			
Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val	
		515					520					525				

Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 530 535 540
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 545 550 555 560
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 565 570 575
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 580 585 590
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 595 600 605
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 610 615 620
 Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
 625 630 635 640
 Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
 645 650 655
 Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
 660 665 670
 Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
 675 680 685
 Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
 690 695 700
 Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr
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 Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
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Phe Phe

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<220>
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 Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
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 Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
 35 40 45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
 50 55 60

Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
 65 70 75 80

Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
 85 90 95

Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
 100 105 110

Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
 115 120 125

Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
 130 135 140

Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
 145 150 155 160

Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
 165 170 175

Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
 180 185 190

Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
 195 200 205

Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
 210 215 220

Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser
 225 230 235 240

Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
 245 250 255

Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
 260 265 270

Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
 275 280 285

His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile
 290 295 300

Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Leu Glu Asn Ile Gln
 305 310 315 320

Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
 325 330 335

Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
 340 345 350

Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
 355 360 365

Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
 370 375 380

Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
 385 390 395 400

Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
 405 410 415

Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
 420 425 430

Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
 435 440 445

Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His
 450 455 460

Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
 465 470 475 480

Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
 485 490 495

Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
 500 505 510

Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
 515 520 525

Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
 530 535 540

Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe
 545 550 555 560

Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575

Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590

Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605

Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
 610 615 620

Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
 625 630 635 640

Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
 645 650 655

Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
 660 665 670

Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
 675 680 685

Gln	Glu	Ser	Leu	Phe	Ile	Ile	Asn	Asn	Phe	Ala	Asn	Ser	Asp	Arg	Pro	690	695	700	
Met	Leu	Ala	Arg	Ala	Phe	Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	705	710	715	720
Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	725	730	735	
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	740	745	750	
Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Lys	755	760	765	
Ile	His	Val	Lys	Asn	Gly	Asp	Phe	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	770	775	780	
His	Val	Ala	Ala	Leu	Val	Ala	Glu	Phe	Leu	His	Arg	Lys	Lys	Leu	Phe	785	790	795	800
Pro	Asn	Gly	Cys	Ser	Ala	Phe	Lys	Lys	Ile	Thr	Pro	Asn	Ile	Asp	Glu	805	810	815	
Glu	Gly	Ala	Met	Lys	Glu	Asp	Ala	Gly	Met	Met	Asp	Val	His	Tyr	Ser	820	825	830	
Glu	Glu	Val	Leu	Leu	Glu	Leu	Leu	Glu	Gln	Cys	Val	Asn	Gly	Leu	Trp	835	840	845	
Lys	Ala	Glu	Arg	Tyr	Glu	Ile	Ile	Ser	Glu	Ile	Ser	Lys	Leu	Ile	Gly	850	855	860	
Pro	Ile	Tyr	Glu	Asn	Arg	Arg	Glu	Phe	Glu	Asn	Leu	Thr	Gln	Val	Tyr	865	870	875	880
Arg	Thr	Leu	His	Gly	Ala	Tyr	Thr	Lys	Ile	Leu	Glu	Val	Met	His	Thr	885	890	895	
Lys	Lys	Arg	Leu	Leu	Gly	Thr	Phe	Phe	Arg	Val	Ala	Phe	Tyr	Gly	Gln	900	905	910	
Ser	Phe	Phe	Glu	Glu	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	915	920	925	
Lys	Leu	Thr	Gly	Leu	Ser	Glu	Ile	Ser	Leu	Arg	Leu	Val	Lys	Leu	Tyr	930	935	940	
Gly	Glu	Lys	Phe	Gly	Thr	Glu	Asn	Val	Lys	Ile	Ile	Gln	Asp	Ser	Asp	945	950	955	960
Lys	Val	Asn	Ala	Lys	Glu	Leu	Asp	Pro	Lys	Tyr	Ala	His	Ile	Gln	Val	965	970	975	
Thr	Tyr	Val	Lys	Pro	Tyr	Phe	Asp	Asp	Lys	Glu	Leu	Thr	Glu	Arg	Lys	980	985	990	
Thr	Glu	Phe	Glu	Arg	Asn	His	Asn	Ile	Ser	Arg	Phe	Val	Phe	Glu	Ala	995	1000	1005	

Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
 1010 1015 1020
 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
 1025 1030 1035 1040
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
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 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
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 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val
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 <223> human CLASP-1

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 Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro
 20 25 30
 Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
 35 40 45
 Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60

Val 65	His	Glu	Asp	Leu	Ala 70	Lys	Asn	Val	Thr	Gly 75	Leu	Leu	Lys	Ser	Asn 80
Asp	Ser	Pro	Thr	Val 85	Lys	His	Val	Leu	Lys 90	His	Ser	Trp	Phe	Phe 95	Phe
Ala	Ile	Ile	Leu	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Asp	Thr	Asn	Lys
			100					105					110		
Ile	Gln	Leu	Pro	Arg	Pro	Gln	Arg	Phe	Pro	Glu	Ser	Tyr	Gln	Asn	Glu
		115					120					125			
Leu	Asp	Asn	Leu	Val	Met	Val	Leu	Ser	Asp	His	Val	Ile	Trp	Lys	Tyr
	130					135					140				
Lys	Asp	Ala	Leu	Glu	Glu	Thr	Arg	Arg	Ala	Thr	His	Ser	Val	Ala	Arg
145					150					155					160
Phe	Leu	Lys	Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Cys	Val	Phe	Lys
				165					170					175	
Met	Val	Asn	Asn	Tyr	Ile	Ser	Met	Phe	Ser	Ser	Gly	Asp	Leu	Lys	Thr
			180					185					190		
Leu	Cys	Gln	Tyr	Lys	Phe	Asp	Phe	Leu	Gln	Glu	Val	Cys	Gln	His	Glu
		195					200					205			
His	Phe	Ile	Pro	Leu	Cys	Leu	Pro	Ile	Arg	Ser	Ala	Asn	Ile	Pro	Asp
	210					215					220				
Pro	Leu	Thr	Pro	Ser	Glu	Ser	Thr	Gln	Glu	Leu	His	Ala	Ser	Asp	Met
225					230					235					240
Pro	Glu	Tyr	Ser	Val	Thr	Asn	Glu	Phe	Cys	Arg	Lys	His	Phe	Leu	Ile
				245					250					255	
Gly	Ile	Leu	Leu	Arg	Glu	Val	Gly	Phe	Ala	Leu	Gln	Glu	Asp	Gln	Asp
		260						265					270		
Val	Arg	His	Leu	Ala	Leu	Ala	Val	Leu	Lys	Asn	Leu	Met	Ala	Lys	His
		275					280					285			
Ser	Phe	Asp	Asp	Arg	Tyr	Arg	Glu	Pro	Arg	Lys	Gln	Ala	Gln	Ile	Ala
	290					295					300				
Ser	Leu	Tyr	Met	Pro	Leu	Tyr	Gly	Met	Leu	Leu	Asp	Asn	Met	Pro	Arg
305					310				315						320
Ile	Tyr	Leu	Lys	Asp	Leu	Tyr	Pro	Phe	Thr	Val	Asn	Thr	Ser	Asn	Gln
			325						330					335	
Gly	Ser	Arg	Asp	Asp	Leu	Ser	Thr	Asn	Gly	Gly	Phe	Gln	Ser	Gln	Thr
			340					345					350		
Ala	Ile	Lys	His	Ala	Asn	Ser	Val	Asp	Thr	Ser	Phe	Ser	Lys	Asp	Val
		355					360					365			
Leu	Asn	Ser	Ile	Ala	Ala	Phe	Ser	Ser	Ile	Ala	Ile	Ser	Thr	Val	Asn
	370					375					380				

His	Ala	Asp	Ser	Arg	Ala	Ser	Leu	Ala	Ser	Leu	Asp	Ser	Asn	Pro	Ser		
385					390					395					400		
Thr	Asn	Glu	Lys	Ser	Ser	Glu	Lys	Thr	Asp	Asn	Cys	Glu	Lys	Ile	Pro		
				405					410					415			
Arg	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Leu	Arg	Phe	Asp	Arg	Leu	Asp		
			420					425					430				
Gln	Ala	Glu	Thr	Arg	Ser	Leu	Leu	Met	Cys	Phe	Leu	His	Ile	Met	Lys		
		435					440					445					
Thr	Ile	Ser	Tyr	Glu	Thr	Leu	Ile	Ala	Tyr	Trp	Gln	Arg	Ala	Pro	Ser		
	450					455					460						
Pro	Glu	Val	Ser	Asp	Phe	Phe	Ser	Ile	Leu	Asp	Val	Cys	Leu	Gln	Asn		
465					470					475					480		
Phe	Arg	Tyr	Leu	Gly	Lys	Arg	Asn	Ile	Ile	Arg	Lys	Ile	Ala	Ala	Ala		
				485					490						495		
Phe	Lys	Phe	Val	Gln	Ser	Thr	Gln	Asn	Asn	Gly	Thr	Leu	Lys	Gly	Ser		
			500					505					510				
Asn	Pro	Ser	Cys	Gln	Thr	Ser	Gly	Leu	Leu	Ala	Gln	Trp	Met	His	Ser		
		515					520					525					
Thr	Ser	Arg	His	Glu	Gly	His	Lys	Gln	His	Arg	Ser	Gln	Thr	Leu	Pro		
	530					535					540						
Ile	Ile	Arg	Gly	Lys	Asn	Ala	Leu	Ser	Asn	Pro	Lys	Leu	Leu	Gln	Met		
545					550					555					560		
Leu	Asp	Asn	Thr	Met	Thr	Ser	Asn	Ser	Asn	Glu	Ile	Asp	Ile	Val	His		
				565					570					575			
His	Val	Asp	Thr	Glu	Ala	Asn	Ile	Ala	Thr	Glu	Gly	Cys	Leu	Thr	Ile		
			580					585					590				
Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln		
		595					600					605					
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr		
	610					615					620						
Met	Leu	Phe	Phe	Gln	Val	Asn	Gln	Ser	Ala	Thr	Ala	Leu	Lys	His	Val		
625					630					635					640		
Phe	Ala	Ser	Leu	Arg	Leu	Phe	Val	Cys	Lys	Phe	Pro	Ser	Ala	Phe	Phe		
				645					650					655			
Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys		
			660					665					670				
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu		
		675					680					685					
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser		
	690					695					700						

Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile	705	710	715	720
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile	725	730	735	
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe	740	745	750	
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	755	760	765	
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val	770	775	780	
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	785	790	795	800
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly	805	810	815	
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile	820	825	830	
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys	835	840	845	
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser	850	855	860	
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro	865	870	875	880
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys	885	890	895	
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val	900	905	910	
Glu	Gln	Leu	Tyr	Met	Cys	Gly	Glu	Phe	Leu	Trp	Lys	Ser	Glu	Arg	Tyr	915	920	925	
Glu	Leu	Ile	Ala	Asp	Val	Asn	Lys	Pro	Ile	Ile	Ala	Val	Phe	Glu	Lys	930	935	940	
Gln	Arg	Asp	Phe	Lys	Lys	Leu	Ser	Asp	Leu	Tyr	Tyr	Asp	Ile	His	Arg	945	950	955	960
Ser	Tyr	Leu	Lys	Val	Ala	Glu	Val	Val	Asn	Ser	Glu	Lys	Arg	Leu	Phe	965	970	975	
Gly	Arg	Tyr	Tyr	Arg	Val	Ala	Phe	Tyr	Gly	Gln	Gly	Phe	Phe	Glu	Glu	980	985	990	
Glu	Glu	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Gly	Leu	995	1000	1005	
Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ala	Asp	Lys	Phe	Gly	1010	1015	1020	

Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055
 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
 1060 1065 1070
 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
 1075 1080 1085
 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
 1090 1095 1100
 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
 1105 1110 1115 1120
 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
 1125 1130 1135
 Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
 1140 1145 1150
 Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
 1155 1160 1165
 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
 1170 1175 1180
 Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
 1185 1190 1195 1200
 Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
 1205 1210 1215
 Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
 1220 1225 1230
 Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn
 1235 1240 1245
 Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
 1250 1255 1260
 Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
 1265 1270 1275 1280
 Ser Ile Ser Ser Ser Ala Glu Val
 1285

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<220>
 <223> human CLASP-3

Thr	Glu	Leu	Ala	Val	Ile	Leu	Asp	Pro	Asp	Ala	Glu	Gly	Leu	Phe	Gly	
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Leu	His	Lys	Lys	Val	Ile	Asn	Met	Val	His	Asn	Leu	Leu	Ser	Ser	His	
			340					345					350			
Asp	Ser	Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala	
		355					360					365				
Met	Leu	Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln	
	370					375					380					
Leu	Tyr	Asp	Phe	Thr	Glu	Thr	His	Asn	Gln	Arg	Gly	Arg	Pro	Ile	Cys	
385					390					395					400	
Ile	Ala	Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln	
				405						410				415		
Thr	Val	Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg	
			420					425					430			
Pro	Gly	Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr	
		435					440					445				
Phe	Ser	Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val	
	450					455					460					
Leu	Lys	Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu	
465					470					475					480	
Ser	Val	Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val	
				485					490					495		
Ser	Cys	Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser	
			500					505					510			
Leu	Thr	Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala	
		515					520					525				
Ile	Leu	Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg	
	530					535					540					
Gly	Gln	Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu	
545					550					555					560	
Asn	Leu	Arg	Trp	Arg	Lys	Asp	Met	Thr	His	Trp	Arg	Gln	Asn	Thr	Glu	
				565					570					575		
Lys	Leu	Asp	Lys	Ser	Arg	Ala	Glu	Ile	Glu	His	Glu	Ala	Leu	Ile	Asp	
			580					585					590			
Gly	Asn	Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu	
		595					600					605				
Ile	Val	Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu	
	610					615					620					
Gly	Gly	Val	Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser	
625					630					635					640	

Ala	Val	Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	
				645					650					655		
Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp	
			660				665						670			
Leu	Cys	Leu	Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile	
		675					680					685				
Arg	Ser	His	Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	
	690					695					700					
Glu	Ile	Gly	Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser	
705					710					715					720	
Leu	Ser	Ser	Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu	
				725				730						735		
Arg	Arg	Ser	Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu	
			740					745					750			
Leu	Arg	Glu	Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn	
		755					760					765				
Leu	His	Met	Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	
	770					775					780					
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr	
785					790					795					800	
Gln	Thr	Ser	Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	
				805					810					815		
Lys	His	Ser	Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val	
			820					825					830			
His	Ser	Ala	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg	
		835					840					845				
Lys	Tyr	Leu	Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn	
	850					855					860					
Val	Leu	Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	
865					870					875					880	
Glu	Gly	Ile	Cys	Ser	Gly	Lys	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	
				885					890					895		
Leu	Leu	Glu	Gln	Ala	Ala	Ala	Ser	Phe	Ser	Met	Ala	Gly	Met	Tyr	Glu	
			900					905					910			
Ala	Val	Asn	Glu	Val	Tyr	Lys	Val	Leu	Ile	Pro	Ile	His	Glu	Ala	Asn	
		915					920					925				
Arg	Asp	Ala	Lys	Lys	Leu	Ser	Thr	Ile	His	Gly	Lys	Leu	Gln	Glu	Ala	
	930					935					940					
Phe	Ser	Lys	Ile	Val	His	Gln	Ser	Thr	Gly	Trp	Glu	Arg	Met	Phe	Gly	
945					950					955					960	

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Met	Asn	Ala	Asp	Thr	Ala	Pro	Thr	Ser	Pro	Cys	Pro	Ser	Ile	Ser	Ser	1	5	10	15
Gln	Asn	Ser	Ser	Ser	Cys	Ser	Ser	Phe	Gln	Asp	Gln	Lys	Ile	Ala	Ser	20	25	30	
Met	Phe	Asp	Arg	Thr	Ser	Arg	Val	Pro	Ala	Ser	Ser	Thr	Ser	Ser	Pro	35	40	45	
Gly	Leu	Leu	Phe	Thr	Glu	Leu	Ala	Ala	Ala	Leu	Asp	Ala	Glu	Gly	Glu	50	55	60	
Gly	Ile	Ser	Glu	Val	Gln	Arg	Lys	Ala	Val	Ser	Ala	Ile	His	Ser	Leu	65	70	75	80
Leu	Ser	Ser	His	Asp	Leu	Asp	Pro	Arg	Cys	Val	Lys	Pro	Glu	Val	Lys	85	90	95	
Val	Lys	Ile	Ala	Ala	Leu	Tyr	Leu	Pro	Leu	Val	Gly	Ile	Ile	Leu	Asp	100	105	110	
Ala	Leu	Pro	Gln	Leu	Cys	Asp	Phe	Thr	Val	Ala	Asp	Thr	Arg	Arg	Tyr	115	120	125	
Arg	Thr	Ser	Gly	Ser	Asp	Glu	Glu	Gln	Glu	Gly	Ala	Gly	Ala	Ile	Thr	130	135	140	
Gln	Asn	Val	Ala	Leu	Ala	Ile	Ala	Gly	Asn	Asn	Phe	Asn	Leu	Lys	Thr	145	150	155	160
Ser	Gly	Ile	Val	Leu	Ser	Ser	Leu	Pro	Tyr	Lys	Gln	Tyr	Asn	Met	Leu	165	170	175	
Asn	Ala	Asp	Thr	Thr	Arg	Asn	Leu	Met	Ile	Cys	Phe	Leu	Trp	Ile	Met	180	185	190	
Lys	Asn	Ala	Asp	Gln	Ser	Leu	Ile	Arg	Lys	Trp	Ile	Ala	Asp	Leu	Pro	195	200	205	
Ser	Thr	Gln	Leu	Asn	Arg	Ile	Leu	Asp	Leu	Leu	Phe	Ile	Cys	Val	Leu	210	215	220	
Cys	Phe	Glu	Tyr	Lys	Gly	Lys	Gln	Ser	Ser	Asp	Lys	Val	Ser	Thr	Gln	225	230	235	240
Val	Leu	Gln	Lys	Ser	Arg	Asp	Val	Lys	Ala	Arg	Leu	Glu	Glu	Ala	Leu	245	250	255	
Leu	Arg	Gly	Glu	Gly	Ala	Arg	Gly	Glu	Met	Met	Arg	Arg	Arg	Ala	Pro	260	265	270	
Gly	Asn	Asp	Arg	Phe	Pro	Gly	Leu	Asn	Glu	Asn	Leu	Arg	Trp	Lys	Lys	275	280	285	
Glu	Gln	Thr	His	Trp	Arg	Gln	Ala	Asn	Glu	Lys	Leu	Asp	Lys	Thr	Lys	290	295	300	
Ala	Glu	Leu	Asp	Gln	Glu	Ala	Leu	Ile	Ser	Gly	Asn	Leu	Ala	Thr	Glu	305	310	315	320

Ala	His	Leu	Ile	Ile	Leu	Asp	Met	Gln	Glu	Asn	Ile	Ile	Gln	Ala	Ser	
				325					330					335		
Ser	Ala	Leu	Asp	Cys	Lys	Asp	Ser	Leu	Leu	Gly	Gly	Val	Leu	Arg	Val	
			340					345					350			
Leu	Val	Asn	Ser	Leu	Asn	Cys	Asp	Gln	Ser	Thr	Thr	Tyr	Leu	Thr	His	
		355					360					365				
Cys	Phe	Ala	Thr	Leu	Arg	Ala	Leu	Ile	Ala	Lys	Phe	Gly	Asp	Leu	Leu	
	370					375					380					
Phe	Glu	Glu	Glu	Val	Glu	Gln	Cys	Phe	Asp	Leu	Cys	His	Gln	Val	Leu	
385					390					395					400	
His	His	Cys	Ser	Ser	Ser	Met	Asp	Val	Thr	Arg	Ser	Gln	Ala	Cys	Ala	
			405						410					415		
Thr	Leu	Tyr	Leu	Leu	Met	Arg	Phe	Ser	Phe	Gly	Ala	Thr	Ser	Asn	Phe	
			420					425						430		
Ala	Arg	Val	Lys	Met	Gln	Val	Thr	Met	Ser	Leu	Ala	Ser	Leu	Val	Gly	
		435					440					445				
Arg	Ala	Pro	Asp	Phe	Asn	Glu	Glu	His	Leu	Arg	Arg	Ser	Leu	Arg	Thr	
	450					455					460					
Ile	Leu	Ala	Tyr	Ser	Glu	Glu	Asp	Thr	Ala	Met	Gln	Met	Thr	Pro	Phe	
465					470					475					480	
Pro	Thr	Gln	Val	Glu	Glu	Leu	Leu	Cys	Asn	Leu	Asn	Ser	Ile	Leu	Tyr	
			485						490					495		
Asp	Thr	Val	Lys	Met	Arg	Glu	Phe	Gln	Glu	Asp	Pro	Glu	Met	Leu	Met	
			500					505					510			
Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Ser	Tyr	Gln	Ala	Ser	Pro	Asp	Leu	
		515					520					525				
Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Glu	Lys	His	Thr	Lys	Lys	Lys	
	530					535					540					
Cys	Tyr	Thr	Glu	Ala	Ala	Met	Cys	Leu	Val	His	Ala	Ala	Ala	Leu	Val	
545					550					555					560	
Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	His	Ser	Tyr	Leu	Pro	Val	Gly	
			565						570					575		
Ser	Val	Ser	Phe	Gln	Asn	Ile	Ser	Ser	Asn	Val	Leu	Glu	Glu	Ser	Val	
			580					585					590			
Val	Ser	Glu	Asp	Thr	Leu	Ser	Pro	Asp	Glu	Asp	Gly	Val	Cys	Ala	Gly	
		595					600					605				
Gln	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	Leu	Leu	Glu	Gln	Ala	Ala	
	610					615					620					
Glu	Leu	Phe	Ser	Thr	Gly	Gly	Leu	Tyr	Glu	Thr	Val	Asn	Glu	Val	Tyr	
625					630					635					640	

Lys	Leu	Val	Ile	Pro	Ile	Leu	Glu	Ala	His	Arg	Glu	Phe	Arg	Lys	Leu	645	650	655	
Thr	Leu	Thr	His	Ser	Lys	Leu	Gln	Arg	Ala	Phe	Asp	Ser	Ile	Val	Asn	660	665	670	
Lys	Asp	His	Lys	Arg	Met	Phe	Gly	Thr	Tyr	Phe	Arg	Val	Gly	Phe	Phe	675	680	685	
Gly	Ser	Lys	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	Lys	Glu	690	695	700	
Pro	Ala	Ile	Thr	Lys	Leu	Pro	Glu	Ile	Ser	His	Arg	Leu	Glu	Ala	Phe	705	710	715	720
Tyr	Gly	Gln	Cys	Phe	Gly	Ala	Glu	Phe	Val	Glu	Val	Ile	Lys	Asp	Ser	725	730	735	
Thr	Pro	Val	Asp	Lys	Thr	Lys	Leu	Asp	Pro	Asn	Lys	Ala	Tyr	Ile	Gln	740	745	750	
Ile	Thr	Phe	Val	Glu	Pro	Tyr	Phe	Asp	Glu	Tyr	Glu	Met	Lys	Asp	Arg	755	760	765	
Val	Thr	Tyr	Phe	Glu	Lys	Asn	Phe	Asn	Leu	Arg	Arg	Phe	Met	Tyr	Thr	770	775	780	
Thr	Pro	Phe	Thr	Leu	Glu	Gly	Arg	Pro	Arg	Gly	Glu	Leu	His	Glu	Gln	785	790	795	800
Tyr	Arg	Arg	Asn	Thr	Val	Leu	Thr	Thr	Met	His	Ala	Phe	Pro	Tyr	Ile	805	810	815	
Lys	Thr	Arg	Ile	Ser	Val	Ile	Gln	Lys	Glu	Glu	Phe	Val	Leu	Thr	Pro	820	825	830	
Ile	Glu	Val	Ala	Ile	Glu	Asp	Met	Lys	Lys	Lys	Thr	Leu	Gln	Leu	Ala	835	840	845	
Val	Ala	Ile	Asn	Gln	Glu	Pro	Pro	Asp	Ala	Lys	Met	Leu	Gln	Met	Val	850	855	860	
Leu	Gln	Gly	Ser	Val	Gly	Ala	Thr	Val	Asn	Gln	Gly	Pro	Leu	Glu	Val	865	870	875	880
Ala	Gln	Val	Phe	Leu	Ala	Glu	Ile	Pro	Ala	Asp	Pro	Lys	Leu	Tyr	Arg	885	890	895	
His	His	Asn	Lys	Leu	Arg	Leu	Cys	Phe	Lys	Glu	Phe	Ile	Met	Arg	Cys	900	905	910	
Gly	Glu	Ala	Val	Glu	Lys	Asn	Lys	Arg	Leu	Ile	Thr	Ala	Asp	Gln	Arg	915	920	925	
Glu	Tyr	Gln	Gln	Glu	Leu	Lys	Lys	Asn	Tyr	Asn	Lys	Leu	Lys	Glu	Asn	930	935	940	
Leu	Arg	Pro	Met	Ile	Glu	Arg	Lys	Ile	Pro	Glu	Leu	Tyr	Lys	Pro	Ile	945	950	955	960

<210> 19
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-6

 <400> 19
 Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
 1 5 10 15

 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

 <210> 20
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-4

 <400> 20
 Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
 1 5 10 15

 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

 <210> 21
 <211> 31
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from canonical DOCK180

 <400> 21
 Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
 1 5 10 15

 Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
 20 25 30

 <210> 22
 <211> 31
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from canonical DOCK2

<400> 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 23

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK3

<400> 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Tyr Val Cys Arg Gly His
20

<210> 24

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA0716

<400> 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Phe Val Cys Arg Gly His
20

<210> 25

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-3

<400> 25

Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
20

<210> 26
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from rat TRG

<400> 26
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45
Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 27
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-1

<400> 27
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30
Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45
Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 28
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-2

<400> 28
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
 35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 50 55 60

<210> 29
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-4

<400> 29
 Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
 1 5 10 15
 Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
 20 25 30
 Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
 35 40 45
 Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
 50 55 60

<210> 30
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-3

<400> 30
 Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
 1 5 10 15
 Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
 20 25 30
 Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 35 40 45
 Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
 50 55 60

<210> 31
 <211> 54
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human KIAA0716

<400> 31

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
1 5 10 15

Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
20 25 30

Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Glu Ser Gln Glu
50

<210> 32

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK3

<400> 32

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
1 5 10 15

Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
20 25 30

Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Asp Tyr Val Asp
50

<210> 33

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK2

<400> 33

Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
35 40 45

<210> 34

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK180

<400> 34

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
35 40 45

Leu Asp Glu His Pro
50

<210> 35

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-1

<400> 35

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
35 40 45

<210> 36

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from rat TRG

<400> 36

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
35 40 45

<210> 37
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human KIAA1058

<400> 37
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 38
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-2

<400> 38
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 39
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-6

<400> 39
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40

<210> 40
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-4

<400> 40
Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
20 25 30
Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
35 40 45

<210> 41
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-3

<400> 41
Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15
Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
20 25 30
Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
35 40 45

<210> 42
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-5

<400> 42
Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15
Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
20 25 30
Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
35 40 45

<210> 43
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human KIAA0716

<400> 43
 Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15
 Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
 35 40 45

<210> 44
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK2

<400> 44
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15
 Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 45
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK3

<400> 45
 Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15
 Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35 40 45

<210> 46
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from canonical DOCK180

<400> 46
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
1 5 10 15
Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
20 25 30
Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
35 40 45

<210> 47
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-1

<400> 47
Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
1 5 10 15
Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
20 25 30
Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
35 40 45
Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
50 55

<210> 48
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from rat TRG

<400> 48
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15
Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30
Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 49
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA1058

<400> 49
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15
Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30
Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45
Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 50
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-2

<400> 50
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15
Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30
Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45
Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 51
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-6

<400> 51
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45
 Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
 50 55

<210> 52
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-3

<400> 52
 Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
 1 5 10 15
 Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
 20 25 30
 Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
 35 40 45
 Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
 50 55

<210> 53
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-4

<400> 53
 Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
 20 25 30
 Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
 35 40 45
 Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
 50 55

<210> 54
<211> 58
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-5

<400> 54

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20 25 30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu
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<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA0716

<400> 55

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Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 56
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<223> Description of Artificial Sequence:DOCK motifs F
and G from canonical DOCK2

<400> 56

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Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
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Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
 35 40 45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 50 55 60

<210> 57
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK3

<400> 57
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 35 40 45
 Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
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<210> 58
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 and G from canonical DOCK180

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Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys
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Ser Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu
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Met Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu
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Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala
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Ala Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys
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ccc agt gtt ctg gtg tcc ttg agg ctg gat ttt cta cga atc atc tgc 712
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 Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu
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Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser	Ala	Val	Tyr	
545					550					555					560	
Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	Lys	Phe	Pro	
				565					570					575		
Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp	Leu	Cys	Leu	
			580					585					590			
Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile	Arg	Ser	His	
		595					600					605				
Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	Glu	Ile	Gly	
		610				615					620					
Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser	Leu	Ser	Ser	
625					630					635					640	
Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu	Arg	Arg	Ser	
				645					650					655		
Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu	Leu	Arg	Glu	
			660					665					670			
Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn	Leu	His	Met	
		675					680					685				
Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	Asp	Pro	Glu	
		690				695					700					
Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr	Gln	Thr	Ser	
705					710					715					720	
Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	Lys	His	Ser	
				725					730					735		
Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val	His	Ser	Ala	
			740					745					750			
Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg	Lys	Tyr	Leu	
		755					760					765				
Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn	Val	Leu	Glu	
		770				775					780					
Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	Glu	Gly	Ile	
785					790					795					800	
Cys	Ser	Gly	Lys	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	Leu	Leu	Glu	
				805					810					815		
Gln	Ala	Ala	Ala	Ser	Phe	Ser	Met	Ala	Gly	Met	Tyr	Glu	Ala	Val	Asn	
			820					825					830			

Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp Ala
 835 840 845
 Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser Lys
 850 855 860
 Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr Phe
 865 870 875 880
 Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln Glu
 885 890 895
 Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His
 900 905 910
 Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu
 915 920 925
 Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn
 930 935 940
 Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr
 945 950 955 960
 Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu Arg
 965 970 975
 Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His Gly
 980 985 990
 Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser His
 995 1000 1005
 Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu Glu
 1010 1015 1020
 Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys Lys
 1025 1030 1035 1040
 Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro Lys
 1045 1050 1055
 Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
 1060 1065 1070
 Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
 1075 1080 1085
 Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
 1090 1095 1100
 Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu Ile
 1105 1110 1115 1120
 Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser Ser
 1125 1130 1135
 Pro

<210> 61
 <211> 755
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 1.1
 sequence of bacterial artificial chromosome BAC8
 using primer C3S3

<220>
 <221> modified_base
 <222> (1)..(755)
 <223> n = g, a, c or t

```
<400> 61
ttttttgaat taatggtgag caaaaactga gcatgttctt taatattttt tctcttagtg 60
aacaatttta tgctagctca tttgttacct tagaaatctt tttctgttgc acatcttaac 120
gcttttccat gtgcctctaa gacaaaatta catgtgttac atctctaaat aaacactgtg 180
gacactcaac acagtttagg tggaattaag agtgaggctc attttaactc ttattttctc 240
agggatggtt gcataagcta gctatatattt caaaggaaac ttgtgatata ttctttgcta 300
gtcattatac atgaagtgtg taatgacagt attgtagatt ttataccaaa gatggaaaga 360
gctttataga taccactgc tattgttatg gctagtaaac ccttagggaa atgccagtta 420
caatcaataa aaaaacaaca gtctggctgg gtgcagtggc tcacacctgt aatctcagca 480
ctttagaagg ccgaggcagg aggatcactt gagatcagga gtttgagacc cagcctgggc 540
aacatagcaa gagcccatat ntacccaaaa aaaatttttt tttaaattaa gctaaaaccc 600
tggnnggcca caaaacctgt agttcccatc tactttggaa aggcttgaag gangggaggg 660
cttgctttga gccccaagaa ngttcaaagg ctngcngnca ggtnntgatt cnacacntgc 720
aactcccgca ttgggtnaac aaaanccaag gaanc 755
```

<210> 62
 <211> 798
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 1.2
 sequence of bacterial artificial chromosome BAC9
 using primer C3S3

<220>
 <221> modified_base
 <222> (1)..(798)
 <223> n = g, a, c or t

```
<400> 62
aattaatggt gagcaaaaac tgagcatggt ctttaatat ttttctctta gtgaacaatt 60
ttatgctagc tcatttggtta ccttagaaat ctttttctgt tgcacatctt aacgcttttc 120
catgtgcctc taagacaaaa ttacatgtgt tacatctcta aataaacact gtggacactc 180
aacacagttt aggtggaatt aagagtgagg ctcatthtaa ctcttatttt ctgagggatg 240
gttgcataag ctagctatat tttcaaagga aacttgtgat acattctttg ctagtcat 300
tacatgaagt gtataatgac agtattgtag attttatacc aaagatggaa agagctttat 360
agataccac tgctattggt ntggctagta aacccttang gaaatgccag ttncaatcaa 420
taaaaaaaca acagtactgg ctgggtgcag tggcttacac ctgtaatctc agcactttat 480
aaggcccnag gcnggaggat cacttnagat ccaggagttt gagaccagcc tgggcaacat 540
ancaagagcc cattatctac caaaaaantt ttttttttaa aattaagcta aacnctgggt 600
ggnacaaacc tgttnngnttc cnatntnctt ttggaaaagc ttangaaggg gagggcttnc 660
tttgganccc caaaaagttn aaagggnttg cagtcagcct ttnaatcac ccnnnggncc 720
tntcgcattg ggattnccaa nangccaang naaccccgnt cntnttttaa aaaantnttt 780
taaagnannt ttnttngn 798
```

<210> 63
 <211> 656
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 2.1
 sequence of bacterial artificial chromosome BAC8
 using primer HC3AS7

<220>
 <221> modified_base
 <222> (1)..(656)
 <223> n = g, a, c or t

<400> 63
 tcttttnngaa aaagattana ttattaattc tatgatatat taacaataca canctctaac 60
 acttggacta tttttaaaat atggcatgta atttaataga tgactgaaat atttttagctt 120
 ctcaaataatt tttttaaagtt ccctacaatg ttttgtattt gcttaaaata aaatanaaaa 180
 accaccatat tacttttcaga aaattatgct agctaacaat aggacaaaaa attctgtgta 240
 tgtcaacaaa aaaaattcaa ccttaaattt ttttttttcc ataaaaaaca gggctacttg 300
 cccaggtgag angtgctgcc gtatgagctc ctcgntagat tgcgcngccg gantgtcggn 360
 ccctncgttt aatataacgg cgtgngcntg taccgcaggc tntgctaggt cgtgntccca 420
 agatatcntn tntancatan tagacgntgg ngncgnntgc atgtggcntn attntngcaa 480
 ttgtnacaat cctagtntgt acntnanagn tcngccnctg tganntcggt gtatagtcng 540
 nggcncgctt gnttctgatg ctgagagcan tnnncnactn ttnnncnccc atctttncnn 600
 ttnnnnnccc ccttttnnat nttttnnntn ncnnnnnnat ntntnaannn accncc 656

<210> 64
 <211> 967
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 2.2
 sequence of bacterial artificial chromosome BAC9
 using primer HC3AS7

<220>
 <221> modified_base
 <222> (1)..(967)
 <223> n = g, a, c or t

<400> 64
 gcgctnccnn ntnntttatc ttctgaaaag actnatatna ttctatgatt ataacattac 60
 acactctaac actggacttn ttaaatatgg atgtaattaa tagatgactg aatatttttag 120
 cttctcaaat atntttaang tccctacaat gtttgnatnt gcttaaaata aaatanaaaa 180
 ccccatatta ctttcagaaa antatgctag ctaacaatag gacanaaaaa ttctgtgtat 240
 gcaacaaaaa aaaattcaac cttnaatctt cttttttttc caatanaaaa cagggtact 300
 ctgccacagg ctggagtcag tggctgatac agctactgca gctcactccg ggctatgtga 360
 ttgcctgcct aagcctcnga gtagtaggct cagggtgccac tacatgccag taatctaaaa 420
 tttatagaga cagggtctgct gtgtgnccag gctggctaac tccgggctaa gcgttcttgc 480
 ctngctctaa atgtgggata cagnatgtat catncatcag ccaaaaagtt aattaanttc 540
 cagatnanta tttgcatcaa agctccaatn tagcttgaag tagaacctgc tcnttggtta 600
 gantatcccg nntgttatgg atcatattan gcnnntgtga tgccgaatgg natctattcc 660
 gggagacana ttactatngg atganagcan atngcccna tgcttntttg taacgctnna 720
 nntaagaacn ttctngacat cgtcatagnt cgaagtnntn ngcganttga tactaanttc 780
 atgntangcc natgactntn gtgattnttg antgnctggg agaacctacn tncccntac 840
 nnatannctn caccctctac tactntnnen ntenctctct anttctactc cacnttatta 900
 tectennect tencatctc ccatentnat tenacgcenc nanacttanc nttnatncac 960

<210> 65
 <211> 722
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 3.1
 sequence of bacterial artificial chromosome BAC8
 using primer C3AS4

<220>
 <221> modified_base
 <222> (1)..(722)
 <223> n = g, a, c or t

<400> 65
 taatgtacat agtgctcatg actgcagatg attcgtagaa aatccagcct caaggacacc 60
 agaacactgg gattcggtaa tgagtaaagc tttgaagaca ccttgtaagc aatgcataag 120
 taagagaaca ccaattgaat ctattatttc ttttaatacta ataccagaat ggcaaattag 180
 aattaaagag atagtacttg gtatccagtt tggggttttgt ggcttaagta gcagtatcac 240
 ctttttccag agttactgct aaaattaaaa attttaaact atcaggttta ctgtataaac 300
 atatttgact aacctaaaag ccacattcct gtatttccaa tatagcatca atatttctac 360
 ttctcataaa acagggaaaa cgtatatcac caaaaataac ttcttattac ttccttctta 420
 aaagaaatta tcaattcttt ttatagcact ttgtgcttac ctgtatttat aatttgtctg 480
 ttttctcagc aacatcataa gctacttgag gagacatact ataaactgat ttaacagcct 540
 tagtgctcct acagcttagc tcaatgtttg acaaataatag gagatcaatg cttaaaggaa 600
 taaaggccag gacaagttct ggtagcaaat agtcataaaa aggttttggg ggaaaagggt 660
 aaaaatggat acatatcggg gtngcaagnt ttttccatgt ggggtgaggt gccccatgcc 720
 tt 722

<210> 66
 <211> 783
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 3.2
 sequence of bacterial artificial chromosome BAC9
 using primer C3AS4

<220>
 <221> modified_base
 <222> (1)..(783)
 <223> n = g, a, c or t

<400> 66
 taacatagtg ctctgactgc agatgattcg tagaaaatcc agcctcaagg acaccagaac 60
 actgggattc ggtaatgagt aaagctttga agacaccttg taagcaatgc ataagtaaga 120
 gaacaccaat tgaatctatt atttctttta tactaatacc agaatggcaa attagaatta 180
 aagagatagt acttggtatc cagtttgggt tttgtggcct aagtagcagt atcacctttt 240
 tccagagtta ctgctaaaat taaaaatttt aaactatcag gtttactgta taaacatatt 300
 tgactaacct aaaagccaca ttcttgtatt tccaatatag catcaatatt tctacttctc 360
 ataaaacagg gaaaacgtat ntcacaaaaa ataacttctt attacttcct tcttaaaaag 420
 aaattatcaa ttcttttttat agcactttgt gcttaccctg nathttataat ttgnctgntt 480
 ttctcagcaa acatcataag ctacttgagg gagacatact attaaacctg attacagcct 540
 ttangtgtcc ctacagctta actcaatgtt ttgcaaaatn tnnggagatc aatggcttta 600
 aagaataaaa gancagggac aagttntggg tngccatnag nacaataaag gttttngggg 660

```

gaaaaggggaa aaaatngatt ncatntcgng gttngcaagg tnttttccat tgnngggngg 720
aggggcccat gccataantt ttaacctttc ttttttngaa gaaattaaac nnttaaagg 780
gtn 783

```

```

<210> 67
<211> 721
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 4.1
      sequence of bacterial artificial chromosome BAC8
      using primer HC3AS6

```

```

<220>
<221> modified_base
<222> (1)..(721)
<223> n = g, a, c or t

```

```

<400> 67
ccagtctgca atatgctgtg cgaagccgat atcaactttg catctttgtc ttgncattcg 60
agaaatcaga cttgtggaag taggagacag cttacagcgt gcacaagctc tcagcagagc 120
atatacgaat gaatcttttc cagggagtta tttatatact acctgagcaa gccactttag 180
ctttgggcag gaacttntgg atgttataag taatacttat atgaataata tgaaattaat 240
atttacttct ttacantct tctcttttcc ttatcttagc ctttatcccc ttgtggaaaa 300
gacactatca atgctagatn ctccaagnc agagaattat gcaggtttgg tcagagaatc 360
gacacagaca tgtttacaga ttcttcttga aatacatatt gtgcacgagt tttttacant 420
atctcaattt agatctcaga cagcatntng actagnnggt ctaggacata gatacatntt 480
tgngaacttc tatagaanaa cntntgcntt aaaaaggagc ttgttngana ngaatnnnct 540
gngaagggcc cgatacgana atttgacttc ggngaaaatt nnnnggattnn taaaaanttc 600
taggnngcac cttnaaaang nntgggnacn ttggnggcgg aaaaaagcc cttcnttttag 660
ntntcccnga aatggaaaag tnccaanttc cnaaaaaaan gggctttgtt nncttnncnan 720
a 721

```

```

<210> 68
<211> 921
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 4.2
      sequence of bacterial artificial chromosome BAC9
      using primer HC3AS6

```

```

<220>
<221> modified_base
<222> (1)..(921)
<223> n = g, a, c or t

```

```

<400> 68
gacgccagct ctgtacacag tctgcaatat gctgtgcgga aggccgatat caactattgc 60
atctttgtct ngncatcgag aaatcagact ctgtggaagn aggcagacaa gactatacag 120
cntgcacana gcatctcagc aggcataataa gaatgaanct tttccaggga gttatttata 180
tactacctga gcaagnactt caacttnggc aggaacttgt ggatgnnttat aagtatactt 240
atatgaataa natngaaatt aatatttaat tcttttactt cttctctttt ccttatctta 300
gcctttatcc cctcgtgaaa aagagcacta atcaatgcta tttnctnccaa gncaggaatt 360
tatagcaggt tggtcgagaa tcgacacgac atgtttacag antcatcttg aatacatnat 420
tgtgcacgag tnttttactc tatctcaaaa tatagatctc agatcgtcta tngantatgn 480
ggttctagga catgattaca tttttnggga acttccatag aataaacntn tacctnaaaa 540

```

```

nangagcctg ttngaaatng aatctactnc taaagggcna gtnccanatt ttacttccgc 600
ganatntcng gatgttacia gtctaggggg nctttagnac gttngatntt tgancggaaa 660
aaagcccttc tannggtcnc ctaatggaag cgccaattcc naanaaggnc tgtgtntntn 720
gacatttacc ngnnccnttt ctaatcaaac ntntctcttct nnnanccnca ncnncnnccct 780
atannccctat cnctcnnctn nntctntcac tctcnnncnt ntcttccntt ctncactntn 840
nnntcnctnn natnnncttc tccnatccnt ctcanntnnt canntccct acnntncnncn 900
tnttaccatc tncncncc t 921

```

```

<210> 69
<211> 628
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 5.1
      sequence of bacterial artificial chromosome BAC8
      using primer C3S6

```

```

<220>
<221> modified_base
<222> (1)..(628)
<223> n = g, a, c or t

```

```

<400> 69
gtatgatccg ccagaccgct gccatggcaa tngtagggac atcggtcctt caactaacia 60
ggcctggcag tttcctnctc acgtcaacgg tcaaaacaat ccttctacag aatttttttt 120
tctngaaaga caaatattta ctaggatatg cccttaaata tatgagatga ttgtatcagc 180
tgatgcaaaa gtgctcagtt ttatttatga aaatatataa gttcccagaa tattaactgt 240
cttctcccaa acagttttta aaaatgatta cctcaagggt tatgggaaaa agccccgtat 300
tctgcattca gaatttggaa aattgcctca ttatagatag ccatntcttt tttttntttt 360
ttttatnctt caagtcttag ggnacatgtg cacaacatgc aggntagtta catatgtata 420
catgtgccat gttggtgtgc tgcacccann aaccgcgaat ttaacattag gtntatctcc 480
aaatgctatc cnttcaccct tcccccatnc cacaacaagg ccccgggcnt tgngatgttc 540
cccttcctgt gccactgtg tntcacattn ccncttcccn cccttantnn ngatgcagaac 600
ntngccngtn gccctntntt tttnnccc 628

```

```

<210> 70
<211> 953
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 5.2
      sequence of bacterial artificial chromosome BAC9
      using primer C3S6

```

```

<220>
<221> modified_base
<222> (1)..(953)
<223> n = g, a, c or t

```

```

<400> 70
ccnctgatga ttatgaaagt gagagcggaa gtatgataag ccagaccggt gccatggcaa 60
tcgcagggac atcggtcctt caactaacia ggcctggcag tttcctcctc acgtcaacgg 120
taaaaacaat cctcctacag aatttttttt tctagaaaga caaatattta ctaggatatg 180
cccttaaata tatgagatga ttgtatcagc ttgatgcaaa aagtgtcagc gtttatattat 240
gaaaatatta aagttccaga atattttaact gtcttctccc aacagtttta aaaaatgata 300
cctcagggtt atggggaaaa aagccccgta ttctgtcatt cagaaatttg gaaaatttgn 360
ctcattatag atagttcatt ttcttttttt tttttttttt ttatacnntt aaagttttta 420

```



```

aggggnacca tgttgcacca aanattgcag gggttngggt accattatgg ttattnccat 480
tggtncceccc antgtttggg gngttggctt tgccaccccc cagngtaaaa ccnnccgntg 540
cgaatttttta aaacaanttt tgggggttat tanttntttc ccaaaaatng gcntttttnc 600
cctttncceccc cctttcnccc ncccnnttcc caacnnanca aggggcccccc cgggtantgg 660
gggaatagnt ttccccccct tncctngnn gggccaattg tggggnnnct ccatttggnn 720
tgcaaanntc ccccaccnt nattgttggg ggngaaacca tttcccgggg ggtttggggg 780
tttttttttg tcccnttgc ccaantaatt tttgcnttga anaaaaagaa tgggggttttc 840
caaagctttt ngtnccatt tgntcccttt anggnncnt tngttcncct tnccanaang 900
ggccaatgtg aaacnncctt tcattttttt ttattggggn ttnccnttat ggn 953

```

```

<210> 71
<211> 683
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 6.1
sequence of bacterial artificial chromosome BAC8
using primer C3S7

```

```

<220>
<221> modified_base
<222> (1)..(683)
<223> n = g, a, c or t

```

```

<400> 71
ttcttgggag cataggtgcc aggcaagaaa tggtagggcg aagccgagga cagctcggta 60
cgtaacacat agcttctcct cctgggtgaga atttcttcaa tttccttgag ttgtatattg 120
taatgatcat tgttgctagt cttcaatgtc aatcctatgc tttttaaaaa gtgttttaag 180
tgtaactgtg aattaacttg aataatcatt tctctgcagt aataaaagt agaattctga 240
tttaggtgag tcagcatacc gccccccccc ccgttttctc tagaaagtct tctctagaaa 300
acgttctcta gaaagtccta tctagaaaac tttctctaga aagtccttat gtgattaata 360
gcatccatcc tcccttttta aatagacttt attttttagt agcagtttta agttcacagc 420
aaaagtgagc aaagggtacag agatttccca tatacccctt agtatgcgta gcctccccca 480
ttattaacat ccccatcaa gagtagtgca tttgttgtaa ctggtgaacc tacattaaca 540
catcatcacc cagagtcgcg agtttacatt agggatcatt catataacat ctatttttac 600
tttttttttt ttagttgaga caagattctc gctctgtcac ccaagctgga gtgcagtccg 660
ngtggtattg nggcttactg ncn 683

```

```

<210> 72
<211> 807
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 6.2
sequence of bacterial artificial chromosome BAC9
using primer C3S7

```

```

<220>
<221> modified_base
<222> (1)..(807)
<223> n = g, a, c or t

```

```

<400> 72
gtgccggcaa gaaatgggtac ggcgaagccg aggacagctc ggtacgtaca caatagcttc 60
tcctcctggg gagaatttct tcaatttcct tgagttgtat attgtaatga tcattgttgc 120
tagtcttcaa tgtcaatcct atgcttttta aaaagtgttt taagtgtaac tnggaattaa 180
cttgaataat catttctctg cagtaataaa agttagaatt ctgatttagg tgagtcagca 240

```



```

taccgcccc cccccggtt tctctagaaa gtcttctcta gaaaacgttc tctagaaagt 300
cctctctaga aaactttctc tagaaagtcc ttatgtgatt aatagcatcc atcctccctt 360
tttaaataag actttatttt tgtagagcag ttttaagttc acagcaaaag tgagcaaagg 420
gcagagattt cccatatacc ccttagtatg cgtagcctcc cccattatta acatccccat 480
cagagtaagn gcatttggtg taactggnga acctacaatt nacacattnt naccacacag 540
tcccgcaggt ttacatttat gggatcattc ccctantaac acctattttt ttactttttt 600
tttttttttag gttgagacaa gaatttttcgg cttcttgtgt acccccaaac tnggtagtag 660
ncnnaccgtc gngnaatttn tggggtttcn tngngnncan tttgtgcnnt cnncttnncn 720
ccnaaagaan ttttttttca cccttttttt tccccnaan anannancct tccccttggn 780
ggangctggg gacttccnca gnggngg 807

```

```

<210> 73
<211> 721
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 7.1
      sequence of bacterial artificial chromosome BAC8
      using primer C3S8

```

```

<220>
<221> modified_base
<222> (1)..(721)
<223> n = g, a, c or t

```

```

<400> 73
caaagtgcag tttatctcaa cactgttttg ctcacagaga gccttggttt caaaggtagg 60
ttattttgta cctgcagtgt tgtcagactt tgtttttttt attaacattg tctaagatca 120
tttgacacat tcattgggta atatatgtag taatatatta atgaatatgt gtagttaaaa 180
tttaaataat aacctaagac ccttaattct tctttgcctc tctactgctg cctgcctttt 240
agaatttttc atttattcga atcaccttta accagtctct gtttgaaaaa cagtaacttg 300
gatgtggaga agggcctgaa attaatagcc aatcttaaat atggggcttc tcttgttttc 360
tcttcacttg gttctgtttt tataaaaaaac tcaatttata aagaattcaa tatataagca 420
attcaacca ctgaaattat tttatgatga atggaaaaga aggtatgtgt ttgttcaact 480
gctttaaatg tttacttctt atatttggtt tcccttagaa atatgtatat tcttaaattt 540
tgaaggtagc tatttcattt taatcatcct agaggatgga atgcanagat gttggatgaa 600
aataacttac gtattatttt gtaataaata taagaattca tatatgggtg attacctaag 660
tggttttatg cacattctga tagaaagctt caccaacaat cccttgntng atatattatt 720
t 721

```

```

<210> 74
<211> 836
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 7.2
      sequence of bacterial artificial chromosome BAC9
      using primer C3S8

```

```

<220>
<221> modified_base
<222> (1)..(836)
<223> n = g, a, c or t

```

```

<400> 74
aagtcagttt atctacaaca ctgttttgct acacagagag ccttggtttc aaaggtaggt 60
tattttgtac ctgcagtgtt gtcagacttt gtttttttta ttaacattgt ctaagatcat 120

```

```

ttgacacatt cattgggttaa tatatgtagt aatatattaa tgaatatgtg tagttaaaat 180
ttaaataata acctaagacc cttaattctt ctttgcctct ctactgctgc ctgcctttta 240
gaatttttca ttatttcgaa tcacctttaa ccagttcttg tttgaaaaac agtaacttgg 300
atgtggagaa gggcctgaaa ttaatagcca atcttaaata tggggccttct cttgntttct 360
cttcacttgg ttctgttttt ataaaaaact caatttataa agaattcaat atataagcca 420
ttcacccact gaaattatth tatgatgaat ggaaaagaaa ggtatgtgtt tggtcacctg 480
ctttaaaatg ngacntcnta atattttggn tttcccctta agaaaatatg tataatcctt 540
aaaantttng aaagggangc tantttcatt ttttnaatca atcctaana ggtattggga 600
atgcncaga ttttttgatt gaaaaanaac cttancgnat ttaatttttn ggnaataaaa 660
taattagnaa ttcntatta tgnttngaag tacctaaagt ggtttttatt gccccatttc 720
nttgatatgn aaagcctttc accaaccaaa tttcccnttg nnaggaatat tatttttttna 780
ngggcctcnt ntttgtgggg ntggaagnaa aaacctttgt tccaaagggt cccnc 836

```

```

<210> 75
<211> 678
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 8.1
      sequence of bacterial artificial chromosome BAC8
      using primer C3S10

```

```

<220>
<221> modified_base
<222> (1)..(678)
<223> n = g, a, c or t

```

```

<400> 75
agtgctagtc ctcagcagca cttgttgctg aatatttgag catgctggag gaccggaaat 60
atcttcctgt gggatgtgta acatttcagg taggaatctt ccagatgtac attaaatcaa 120
ggtatatctt tttttgggtt tagcttttct cactgggtgt tagatttttt tagtttataa 180
ggaaagctta aagacttaag ccaatgcttc acaagggtgaa ttaacatttc acagtgattg 240
tcattaatac atttttaagg agtacttctt gttgattctc tttccacagt ttcttacctc 300
tgaattatca gcactatgct tattttattct ctttggcttt actgncttgn aatcccgtta 360
catactttta catctatgga aatgtattac tgataatcag aattcagtag aaattcttaa 420
ttggctttta cttcacatag cagatatacc aacattctct attccctaca taaaatatta 480
agattatttt atgactaata cccatgactc acagatgagt ttgccctcta gtaggggtcat 540
aattctgacc cactagttga attctctgct taccaagagn caggatgct tgctttttct 600
tcaaaacctg ttaaatagta ggnttgggga tattntaaaa attaggtaaa tggatatatc 660
tctggtggaa ancagaan 678

```

```

<210> 76
<211> 825
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 8.2
      sequence of bacterial artificial chromosome BAC9
      using primer C3S10

```

```

<220>
<221> modified_base
<222> (1)..(825)
<223> n = g, a, c or t

```

```

<400> 76
cagcagcact tggtgctgaa tatttgagca tgctggagga ccggaaatat cttcctgtgg 60

```

gatgtgtaac	atttcaggta	ggaatcttcc	agatgtacat	taaatcaagg	tatatctttt	120
tttggtttta	gcttttctca	ctgggtgttta	gatttttttta	gtttataagg	aaagcttaaa	180
gacttaagcc	aatgcttcac	aagggtgaatt	aacatttcac	agtgattgtc	attaatacat	240
ttttaaggag	tacttcttgt	tgattctctt	tccacagttt	cttacctctg	aattatcagc	300
actatgctta	tttattctct	ttgtctttac	tgccttgtaa	tccgttacat	actttaacat	360
ctatggaaat	gtattactga	taatcagaat	tcagtagaaa	ttcttaattg	gcttnttact	420
tcacatagca	gatntacca	cattctctat	tccctacata	aaatattagg	attattttat	480
gactaatacc	atgactcaca	gattgagttt	gccctctant	agggtncata	atttctgacc	540
cactagttga	attctctgct	taccaaaggt	canttatgcc	tttgcttttt	cttcaaaacc	600
ctgnttaatt	aggnacggct	ttggagataa	tttataaaaa	atttcaagct	naaantggnt	660
tattattcnt	tccnnggttg	aaaaaaccca	ggaattggca	caaannaana	aaaagnttat	720
tccnggtttc	tttncggnaa	aaaaacccaa	aatcttnga	aattgttttt	taccaaaaan	780
gacctccncn	gggaaaaagg	gngtaaattt	nttcntaaa	aacnn		825

<210> 77
 <211> 904
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 9.1
 sequence of bacterial artificial chromosome BAC9
 using primer C3S11

<220>
 <221> modified_base
 <222> (1)..(904)
 <223> n = g, a, c or t

<400> 77						
ttcctattca	tgaagcta	cgggatgcaa	agaaactatc	cacaattcat	ggtaaacttc	60
aagaagcatt	cagcaaaatt	gttcatcagg	taatgattcc	aatttctagc	ttcactataa	120
agggaaaaaa	ctgtctgaaa	gcattaatgt	tgttttgcac	tgatgtcaaa	ctagatcccg	180
tgaaatgacc	attttaatac	gactacaaat	gagcgggtcaa	aatgatagtt	catggccaaa	240
gcaaagctca	ttaacaataa	aaatgaattc	acctaaagta	aatgggtgatc	atcataaact	300
ttctgcatag	cttttttttt	ttcatttttg	aattattaat	taagcaagtt	tttaaaaatt	360
gtgattttct	gtttcacaag	gnaagatcat	aagttgnnga	atctcatttt	taaaaattga	420
taccctattn	cttttgctgn	ggaaaantgg	aagtttttta	atattttcaa	ggtttttttt	480
aaaattnaaa	tggattgtgg	aaaacctttt	aatnaattt	aaaacctacc	taaaatantt	540
tttttaaatg	nccnngccan	ctggaacctn	tttatttttt	tcccctagga	atgggttttac	600
ccaaatccat	tcccttttga	ataatatatt	tccctnaatt	ncccaaaaaa	ntttttnttt	660
ttttgggngg	aaaaaatant	tggaaaatta	aaaaaatggg	gggtggggccn	taaatgggga	720
ttatttttaa	atttcctaaa	aaagggantt	ttccatttac	ctttnaatcc	tttttgggng	780
gnttcnattt	attggggaat	cctncncttt	ttntnncncc	ttaaaaaant	tagggcctnc	840
caaaatttta	aaccntttaa	tttttnaaaa	nggaaagggn	cccctttctt	ngcccgggtg	900
gttt						904

<210> 78
 <211> 681
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 10.1
 sequence of bacterial artificial chromosome BAC8
 using primer C3S12

<220>
 <221> modified_base
 <222> (1)..(681)
 <223> n = g, a, c or t

<400> 78
 tacagattgg aggtgaatgc tgtgggtgggt cataaaatgt catcttttagt ttgtattctc 60
 tctgatgatt agactttcag atccagatct aatcatttag taagccagat cttgccaaat 120
 aaactactcc gttagagaat aaggactttt aatagttaca ataatactct ttcaaactct 180
 ttatggcagc aataaaatag taatattgtc tattttttga gactattttc acacatatat 240
 tagaaacccc tgtatccttc agaattactg cgacttaacg gagaaatata tagtataatc 300
 ccacattttg ttgaaaaaga caaagaatta agtagtagct aataattgaa ctagaaccag 360
 aaccctaaga aattttctgac ccaagcatat tatctctttg gcttaactgg ttccagggtg 420
 ggtttcttta gaacgtaaaa gcctgaaatc acaccttaaa aacacttcct ttaaccttta 480
 taattttctta attttcacca taaatgattg cgttttatat ttactggggc taactagnat 540
 tttctgntat aggtattctt tccaaccttt ctctattttt tgttactcaa agtgtagtgg 600
 atggaccgga agcattggggg ttcacctggg agaatgggtg gnaatgcaga acccttagac 660
 cccaccccag cccctgtgaa a 681

<210> 79
 <211> 879
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 10.2
 sequence of bacterial artificial chromosome BAC9
 using primer C3S12

<220>
 <221> modified_base
 <222> (1)..(879)
 <223> n = g, a, c or t

<400> 79
 cagatagtag gtgaatgctg tgggtggttca taaaatgtca tcttttagttt gtattctctc 60
 tgatgattag acttttcagat ccagatctaa tcatttagta agccagatct tgccaaataa 120
 actactccgt tagagaataa ggacttttaa tagttacaat aatactcttt caaatctttt 180
 atggcagcaa taaaatagta atattgtcta ttttttgaga ctattttcac acatatatta 240
 gaaacccctg tatccttcag aattactgcg acttaacgga gaaatatata gtataatccc 300
 acattttggt gaaaaagaca aagaattaag tagtagctaa taatttgaac tagaaccaga 360
 accctaagaa atttctgacc caagcatatt atctcttttg cttaactggt tccaggngag 420
 gtatcttttag aacgtnaaag cctgaaatca caccttaaaa acacttnctt taacccttta 480
 taanttnctt aatttttcacc cataaaatng attgcngttt tatattttac ctnggggncta 540
 nacctnaggc aatttttctg ggtcataagg gaaatttctt tttcccaaac ctttttcttc 600
 ttattttggt gggncacctc ccaaaagggtg ntcngttggg gnttngggnc cccgngaaag 660
 gccatttggg ggnttcaccc ccggggggang atttggtttt ggaaaatngt cnnnaaaacc 720
 ttccnnaccc ccnncccccn ggcccccntg nnnngaaatc caaaaggatc ttgncnattt 780
 ttttanccaa angancnccc ccnaggngng gattttngtt atttcccaa naangangtaa 840
 ggttnttggc ctttnggggc nttgggtggt tttnttttnn 879

<210> 80
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 11.1
 sequence of bacterial artificial chromosome BAC9
 using primer HC3AS3

<220>
 <221> modified_base
 <222> (1)..(786)
 <223> n = g, a, c or t

<400> 80
 ctgangtgtn gcaangccac tcctgtgtct tttctgcatg tcctcaatag caacttcaat 60
 cgggtgtaag atgatctgag tnanngagca tctgttanat cagngtactg actgaaacta 120
 tttaatgaac tttatgtata atcaactgaa attaganaaa aaaaagatca atngtaaact 180
 tcatgtaaca ataaaattcc aaacttggat tctaaatgaa nnaaaanant caacctttaa 240
 agaaaagctg ggggtgaata agggcttaga aaagangtan aaaatganga ctcaaaatgg 300
 taaaggggtct aatatgnatg gataaggatg gacatatctt cggactctga gtgggtgtaca 360
 tggcttgatg attgctcact atgtgtgnca ttatggctac ctctctttag gcatgcctgt 420
 taantaggaa gctgaactan caaagnctct tngatgtatn antcctgccg ctnaagaagg 480
 ggncgcntga nncaaagatg ttgcnatgtn tctgctatna tngnaagnn tcctngantn 540
 nttcnganaa anctctcnan gagnctagtt tacatncggt cagngtctt tgcacctcct 600
 gngcatctcc cgtanttcac cctcatttna centnanttt ataannannn agcccacntn 660
 ncctataggg nactnacgn nttcccnnta ntcantnna gacaattttt tnnccgcccc 720
 tectnntect tectnncttc cncncnnenn cectntntct ntnccccnc cnnttcttan 780
 cttntct 786

<210> 81
 <211> 933
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 12.1
 sequence of bacterial artificial chromosome BAC9
 using primer C3S15

<220>
 <221> modified_base
 <222> (1)..(933)
 <223> n = g, a, c or t

<400> 81
 tgtgaaaaga tctattggaa aacaacatgg aatggaattc tggaaattat tattnattga 60
 agaatgcagt ggccaagaaa atatcaaag tagattgtta acgcttgaga atcatggcta 120
 tggtttctaa tgttctggta acaagctgtt atcttttaag acattttaat gactcaaagg 180
 tacactatac atttaccatt atttatacca tagctaagg taaaaattta ttcactttaa 240
 gtctcgatatt tttaatttat attaccattt atagattcat tttggaacca ttttaaatgt 300
 agtaatgctt atttttaaagg tactattaaa tatgtgaatg tttacactaa ttttaccgag 360
 tgggacttca aaatttttat tattgacaat ggctgagaac aattnaaggg tttgactcna 420
 gaactanttc caaacctagc agaataaaaa tcatagatag ccccaaatta atgagtttgg 480
 gnaactgtnt caaagttttt ttccatttac atacccaaaa acaggaaatt ttagaatttg 540
 ccngaacctt taccttaaga naaaaacct tttgtgntna aaaatntant nttaaaattc 600
 ccggggggan taatcttaat naccgccggg ggggccannc nccccnttat aactttggaa 660
 tttaaaaatt cntttttnt ncaaccccaa actgnantng ggtnttttn aaggaaaacc 720
 tttccactng gaagttnnct tttagggncc nancctncna naaanngggg aanattggga 780
 agtcttcccc ttcnttnggg gggngnccca aaaaattctt aataaaancc ccggggctcc 840
 catnttagn attttttttt ttggccccac actgtgttna ttaaancccc ncntgctaaa 900
 aatttttnnn gaaaanacct naaccttct nna 933

<210> 82
<211> 100
<212> DNA
<213> Homo sapiens

<220>
<223> exon 60270-20370

<400> 82
cgccgcagcc gccgccgccg tcgccgtcgc cgcagcagcc atggccgagc gccgcgcctt 60
cgcccagaag atcagcaggt aaatatccgg cgtggggcgc 100

<210> 83
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<223> exon 85360-85510

<400> 83
gtttttgctt tcttcattgt agaacggtgg cagccgaagt taggaagcag atctccggac 60
aatatagtgg ttctcccaa ctgctcaaaa accttaatat tggtggcaat atatcccatc 120
acaccacagt aagtaacgta ttcaaaatat a 151

<210> 84
<211> 220
<212> DNA
<213> Homo sapiens

<220>
<223> exon 94500-94720

<400> 84
tcttatccca actttttaca aaggtgcccc ttaccgaagc agtagatcca gtggatttgg 60
aagattacct cattactcat cctttggctg tggattctgg gcctttacgg gatttgattg 120
aatttcctcc agatgatatt gaagttgttt atagtcctcg ggactgcaga actcttgttt 180
cagctgtacc tgaagaaagg taaggagaca ttgacttatt 220

<210> 85
<211> 111
<212> DNA
<213> Homo sapiens

<220>
<223> exon 94870-94980

<400> 85
tattttcctt tttaaaatag tgaaatggat ccacatgtta gagactgtat aagaagttat 60
acagaagact gggcaattgt catcagaaag taagttatat gtttattaca a 111

<210> 86
<211> 180
<212> DNA
<213> Homo sapiens

<220>
 <223> exon 100110-100290

<400> 86
 atttatttaa ctttttttct ttaatagata tcataaattg ggaacaggat ttaatcccaa 60
 tacattagat aaacagaaag aaaggcaaaa aggtttgcca aaacaagttt ttgaatctga 120
 tgaagctcca gatggcaaca gctaccagga tgatcaagta atacttttat tcttaaataa 180

<210> 87
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 100340-100600

<400> 87
 atattttaatg ttttgcata caggatgacc ttaaaagacg ttcaatgtca atagatgata 60
 cccaagggg tagctgggccc ttagtatctt ttgacttgaa aaattcactt cctgatgctt 120
 tgcttcccaa ttactttgat cgaactccaa atgaagaaat agaccgtcag aatgatgacc 180
 aaaggaaatc aaaccgtcac aaagaacttt ttgctttgca tccatcacca gatgaggtat 240
 agatgtttgc atataaagaa 260

<210> 88
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 100880-101020

<400> 88
 ttttgggtggt gctttttcaat ttgtaggaag aaccaataga acggcttagt gttcctgata 60
 tacccaaaga acatttttgt caaagacttc ttgtaaaatg cttatcactc aagtgagtat 120
 ttattttcttt tacttacaac t 141

<210> 89
 <211> 111
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 112010-112120

<400> 89
 tttttcttca taaaggtttg aaattgaaat tgaaccatt tttgcaagtt tggctttata 60
 tgatgtcaag gaaaagaaaa aggtaagatt atataatttg accatagtta t 111

<210> 90
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 113680-113880

<400> 90
aagtttaaca tactaatatt ttttagatTT cagaaaactt ttattttgac ctttaattctg 60
agcagatgaa agggttgtta cgtccacatg taccacctgc tgccattact accctggcaa 120
gatcagcaat tttttctatc acttattcctt cccaagatgt ttttcttgta ataaagggtga 180
gaataatggt aaatatattt g 201

<210> 91
<211> 140
<212> DNA
<213> Homo sapiens

<220>
<223> exon 115020-115160

<400> 91
ttaatcttaa ctttttttgc ctttgacagc tagaaaaagt cctacagcaa ggagacattg 60
gagagtgtgc agaaccatat atgattttca aagaagcaga tgccaccaag gtagaatgtt 120
atgcttctca tttccgccac 140

<210> 92
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<223> exon 117200-117410

<400> 92
atgtataaag ttctgttttg cagaataaag aaaaactgga gaaactgaag agtcaagcag 60
atcagttttg ccaaagactt gggaaatatt gcatgccttt tgcttggact gcaatccatt 120
taatgaatat tgtagcagt gctgggagtt tggaaagaga ttctacagaa gtagaaatca 180
gtactggagg taagagtgtt tcatacaaaa c 211

<210> 93
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<223> exon 123200-12396

<400> 93
aaaatgaatt ttttttttaa ttcttttgta gaacgaaaag ggtcttggtc agagaggagg 60
aattctagta ttgttggcag acgatcactt gaaaggacaa caagtggaga tgatgcttgt 120
aacttgacga gctttcgacc agctactctc acagtgacaa attttttttaa gcaggatttg 180
ttctgtcatg taggaatttt 200

<210> 94
<211> 94
<212> DNA
<213> Homo sapiens

<220>
<223> next part of CLASP starting

<400> 94
gaaggagacc gcttaagtga tgaagatctc tacaaattcc ttgctgatat gagaaggcca 60

tcttctgtct tacggcgact aagacctatt acag

94

<210> 95
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<223> exon 5560-5710

<400> 95
ctttttcctc tattattgaa atcaggaagg agaccgctta agtgatgaag atctctacaa 60
attccttgct gatatgagaa ggccatcttc tgtcttacgg cgactaagac ctattacagg 120
tatttaaaaa ttttgagtag aaatgggtgc a 151

<210> 96
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<223> exon 6680-6900

<400> 96
ttacattggt ttttaatat taatttgcag ctcagctcaa gatagacatt tctcccgcac 60
ctgaaaatcc ccattattgc ctaactccgg agctgcttca agtgaagctt taccctgaca 120
gtagagttag acctaccaga gaaatcttag agtttcccgc aagggatgtt tatgttccaa 180
acactactta caggtaagag attttaattt ggagaattct g 221

<210> 97
<211> 156
<212> DNA
<213> Homo sapiens

<220>
<223> exon 38920-39075

<400> 97
gtatttacta tcatctatac tgttgctttc acagaaatct tctctacata taccctcaga 60
gtcttaattt tgccaatcgt caagggttctg ctagaaatat aacagtgaag gtccagttta 120
tgtatggaga ggatccaagc aatgccatgc cggtaa 156

<210> 98
<211> 2349
<212> DNA
<213> Homo sapiens

<220>
<223> putative promoter region for human CLASP-3,
genomic sequence upstream of human CLASP-3 5'
terminus

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Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
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Arg	Thr	Leu	Gln	Pro	Ser	Leu	Pro	Glu	Glu	Gly	Val	Glu	Leu	Asp	Pro	35	40	45	
His	Val	Arg	Asp	Cys	Val	Gln	Thr	Tyr	Ile	Arg	Glu	Trp	Leu	Ile	Val	50	55	60	
Asn	Arg	Lys	Asn	Gln	Gly	Ser	Pro	Glu	Ile	Cys	Gly	Phe	Lys	Lys	Thr	65	70	75	80
Gly	Ser	Arg	Lys	Asp	Phe	His	Lys	Thr	Leu	Pro	Lys	Gln	Thr	Phe	Glu	85	90	95	
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Ala	Arg	Arg	Thr	Asn	Arg	Gln	Ala	Glu	Leu	Phe	Ala	Leu	Tyr	Pro	Ser	165	170	175	
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Val	Lys	Ser	Ile	Pro	Gly	Leu	Leu	Arg	Leu	Glu	Ile	Ser	Thr	Ala	Pro	
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Glu	Ile	Ile	Asn	Cys	Cys	Leu	Thr	Pro	Glu	Met	Leu	Pro	Val	Lys	Pro	
	450					455				460						
Phe	Pro	Glu	Asn	Arg	Thr	Arg	Pro	His	Lys	Glu	Ile	Leu	Glu	Phe	Pro	
465					470				475						480	
Thr	Arg	Glu	Val	Tyr	Val	Pro	His	Thr	Val	Tyr	Arg	Asn	Leu	Leu	Tyr	
				485					490					495		
Val	Tyr	Pro	Gln	Arg	Leu	Asn	Phe	Val	Asn	Lys	Leu	Ala	Ser	Ala	Arg	
			500					505					510			
Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn	
		515				520						525				
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln	
	530					535					540					
Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr	
545					550				555						560	
Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His	
				565				570						575		

Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala			
			580					585					590					
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn			
		595					600					605						
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys			
	610					615					620							
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln			
625					630					635					640			
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile			
			645						650					655				
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu			
			660					665					670					
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro			
		675					680					685						
Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu			
	690					695					700							
Leu	Lys	Leu	Ser	Ile	Ile	Cys	Leu	Asn	Ser	Ser	Arg	Leu	Glu	Pro	Leu			
705					710					715					720			
Val	Leu	Phe	Leu	His	Leu	Val	Leu	Asp	Lys	Leu	Phe	Gln	Leu	Ser	Val			
				725					730					735				
Gln	Pro	Met	Val	Ile	Ala	Gly	Gln	Thr	Ala	Asn	Phe	Ser	Gln	Phe	Ala			
			740					745					750					
Phe	Glu	Ser	Val	Val	Ala	Ile	Ala	Asn	Ser	Leu	His	Asn	Ser	Lys	Asp			
		755					760					765						
Leu	Ser	Lys	Asp	Gln	His	Gly	Arg	Asn	Cys	Leu	Leu	Ala	Ser	Tyr	Val			
	770					775					780							
His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser			
785					790					795					800			
Gly	Ala	Pro	Thr	Ala	Leu	Leu	Asp	Pro	Arg	Ser	Tyr	His	Thr	Tyr	Gly			
				805					810					815				
Arg	Thr	Ser	Ala	Ala	Ala	Val	Ser	Ser	Lys	Leu	Leu	Gln	Ala	Arg	Val			
			820					825					830					
Met	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Gly	Thr	His	Ser	Ala	Ala	Asp			
	835						840					845						
Glu	Glu	Val	Lys	Asn	Ile	Met	Ser	Ser	Lys	Ile	Ala	Asp	Arg	Asn	Cys			
	850					855					860							
Ser	Arg	Met	Ser	Tyr	Tyr	Cys	Ser	Gly	Ser	Ser	Asp	Ala	Pro	Ser	Ser			
865					870					875					880			
Pro	Ala	Ala	Pro	Arg	Pro	Ala	Ser	Lys	Lys	His	Phe	His	Glu	Glu	Leu			
				885					890					895				

Ala	Leu	Gln	Met	Val	Val	Ser	Thr	Gly	Met	Val	Lys	Ser	Met	Ala	Gln	900	905	910	
His	Val	His	Asn	Met	Asp	Lys	Arg	Asp	Ser	Phe	Arg	Arg	Thr	Arg	Phe	915	920	925	
Ser	Asp	Arg	Phe	Met	Asp	Asp	Ile	Thr	Thr	Ile	Val	Asn	Val	Val	Thr	930	935	940	
Ser	Glu	Ile	Ala	Ala	Leu	Leu	Val	Lys	Pro	Gln	Lys	Glu	Asn	Glu	Gln	945	950	955	960
Ala	Glu	Lys	Met	Asn	Ile	Ser	Leu	Ala	Phe	Phe	Leu	Tyr	Asp	Leu	Leu	965	970	975	
Ser	Leu	Met	Asp	Arg	Gly	Phe	Val	Phe	Asn	Leu	Ile	Arg	His	Tyr	Cys	980	985	990	
Ser	Gln	Leu	Ser	Ala	Lys	Leu	Ser	Asn	Leu	Pro	Thr	Leu	Ile	Ser	Met	995	1000	1005	
Arg	Leu	Glu	Phe	Leu	Arg	Ile	Leu	Cys	Ser	His	Glu	His	Tyr	Leu	Asn	1010	1015	1020	
Leu	Asn	Leu	Phe	Phe	Met	Asn	Ala	Asp	Thr	Ala	Pro	Thr	Ser	Pro	Cys	1025	1030	1035	1040
Pro	Ser	Ile	Ser	Ser	Gln	Asn	Ser	Ser	Ser	Cys	Ser	Ser	Phe	Gln	Asp	1045	1050	1055	
Gln	Lys	Ile	Ala	Ser	Met	Phe	Asp	Leu	Thr	Ser	Glu	Tyr	Arg	Gln	Gln	1060	1065	1070	
His	Phe	Leu	Thr	Gly	Leu	Leu	Phe	Thr	Glu	Leu	Ala	Ala	Ala	Leu	Asp	1075	1080	1085	
Ala	Glu	Gly	Glu	Gly	Ile	Ser	Lys	Val	Gln	Arg	Lys	Ala	Val	Ser	Ala	1090	1095	1100	
Ile	His	Ser	Leu	Leu	Ser	Ser	His	Asp	Leu	Asp	Pro	Arg	Cys	Val	Lys	1105	1110	1115	1120
Pro	Glu	Val	Lys	Val	Lys	Ile	Ala	Ala	Leu	Tyr	Leu	Pro	Leu	Val	Gly	1125	1130	1135	
Ile	Ile	Leu	Asp	Ala	Leu	Pro	Gln	Leu	Cys	Asp	Phe	Thr	Val	Ala	Asp	1140	1145	1150	
Thr	Arg	Arg	Tyr	Arg	Thr	Ser	Gly	Ser	Asp	Glu	Glu	Gln	Glu	Gly	Ala	1155	1160	1165	
Gly	Ala	Ile	Asn	Gln	Asn	Val	Ala	Leu	Ala	Ile	Ala	Gly	Asn	Asn	Phe	1170	1175	1180	
Asn	Leu	Lys	Thr	Ser	Gly	Ile	Val	Leu	Ser	Ser	Leu	Pro	Tyr	Lys	Gln	1185	1190	1195	1200
Tyr	Asn	Met	Leu	Asn	Ala	Asp	Thr	Thr	Arg	Asn	Leu	Met	Ile	Cys	Phe	1205	1210	1215	

Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
 1220 1225 1230
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
 1235 1240 1245
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
 1250 1255 1260
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
 1265 1270 1275 1280
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
 1285 1290 1295
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
 1300 1305 1310
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
 1315 1320 1325
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
 1330 1335 1340
 Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
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 Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
 1365 1370 1375
 Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
 1380 1385 1390
 Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
 1395 1400 1405
 Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
 1410 1415 1420
 His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
 1425 1430 1435 1440
 Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
 1445 1450 1455
 Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
 1460 1465 1470
 Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
 1475 1480 1485
 Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
 1490 1495 1500
 Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
 1505 1510 1515 1520
 Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
 1525 1530 1535

Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
 1540 1545 1550
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
 1555 1560 1565
 Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
 1570 1575 1580
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
 1585 1590 1595 1600
 Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
 1605 1610 1615
 Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
 1620 1625 1630
 Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 1635 1640 1645
 Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
 1650 1655 1660
 Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
 1665 1670 1675 1680
 Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
 1685 1690 1695
 Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
 1700 1705 1710
 Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
 1715 1720 1725
 Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740
 Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760
 Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775
 Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu
 1780 1785 1790
 Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
 1795 1800 1805
 Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
 1810 1815 1820
 Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
 1825 1830 1835 1840
 Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
 1845 1850 1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
 1860 1865 1870
 Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
 1875 1880 1885
 Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
 1890 1895 1900
 Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
 1905 1910 1915 1920
 Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
 1925 1930 1935
 Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
 1940 1945 1950
 Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys
 1955 1960 1965
 Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu
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 Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His
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 Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 2005 2010 2015

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 Ala Glu Val Arg Lys Gln Ile Ser Gly Gln Tyr Ser Gly Ser Pro Gln
 20 25 30
 Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr
 35 40 45
 Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
 50 55 60
 Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
 65 70 75 80
 Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
 85 90 95
 Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
 100 105 110

Val	Arg	Asp	Cys	Ile	Arg	Ser	Tyr	Thr	Glu	Asp	Trp	Ala	Ile	Val	Ile	
		115					120					125				
Arg	Lys	Tyr	His	Lys	Leu	Gly	Thr	Gly	Phe	Asn	Pro	Asn	Thr	Leu	Asp	
	130					135					140					
Lys	Gln	Lys	Glu	Arg	Gln	Lys	Gly	Leu	Pro	Lys	Gln	Val	Phe	Glu	Ser	
145					150					155					160	
Asp	Glu	Ala	Pro	Asp	Gly	Asn	Ser	Tyr	Gln	Asp	Asp	Gln	Asp	Asp	Leu	
				165					170					175		
Lys	Arg	Arg	Ser	Met	Ser	Ile	Asp	Asp	Thr	Pro	Arg	Gly	Ser	Trp	Ala	
			180				185						190			
Cys	Ser	Ile	Phe	Asp	Leu	Lys	Asn	Ser	Leu	Pro	Asp	Ala	Leu	Leu	Pro	
		195					200					205				
Asn	Leu	Leu	Asp	Arg	Thr	Pro	Asn	Glu	Glu	Ile	Asp	Arg	Gln	Asn	Asp	
	210					215					220					
Asp	Gln	Arg	Lys	Ser	Asn	Arg	His	Lys	Glu	Leu	Phe	Ala	Leu	His	Pro	
225					230					235					240	
Ser	Pro	Asp	Glu	Glu	Glu	Pro	Ile	Glu	Arg	Leu	Ser	Val	Pro	Asp	Ile	
				245					250					255		
Pro	Lys	Glu	His	Phe	Gly	Gln	Arg	Leu	Leu	Val	Lys	Cys	Leu	Ser	Leu	
			260					265					270			
Lys	Phe	Glu	Ile	Glu	Ile	Glu	Pro	Ile	Phe	Ala	Ser	Leu	Ala	Leu	Tyr	
		275					280					285				
Asp	Val	Lys	Glu	Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu	
	290					295					300					
Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	Pro	His	Val	Pro	Pro	Ala	
305					310					315					320	
Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Ile	Thr	Tyr	Pro	
				325					330					335		
Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	
			340					345					350			
Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	Met	Ile	Phe	Lys	Glu	Ala	
		355					360					365				
Asp	Ala	Thr	Lys	Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Lys	Ser	Gln	Ala	
	370					375					380					
Asp	Gln	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp	
385					390					395					400	
Thr	Ala	Ile	His	Leu	Met	Asn	Ile	Val	Ser	Ser	Ala	Gly	Ser	Leu	Glu	
				405					410					415		
Arg	Asp	Ser	Thr	Glu	Val	Glu	Ile	Ser	Thr	Gly	Glu	Arg	Lys	Gly	Ser	
			420					425					430			

Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	Glu	Asn	Asn	Leu	Glu	Asn	
		755					760				765					
Glu	Leu	Lys	Ser	Ser	Ile	Ser	Ala	Leu	Asn	Ser	Ser	Gln	Leu	Glu	Pro	
	770					775					780					
Val	Val	Arg	Phe	Leu	His	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Leu	Leu	Val	
785					790					795					800	
Ile	Arg	Pro	Pro	Val	Ile	Ala	Gly	Gln	Ile	Val	Asn	Leu	Gly	Gln	Ala	
				805					810					815		
Ser	Phe	Glu	Ala	Met	Ala	Ser	Ile	Ile	Asn	Arg	Leu	His	Lys	Asn	Leu	
			820					825					830			
Glu	Gly	Asn	His	Asp	Gln	His	Gly	Arg	Asn	Ser	Leu	Leu	Ala	Ser	Tyr	
		835					840					845				
Ile	His	Tyr	Val	Phe	Arg	Leu	Pro	Asn	Thr	Tyr	Pro	Asn	Ser	Ser	Ser	
	850					855					860					
Pro	Gly	Pro	Gly	Gly	Leu	Gly	Gly	Ser	Val	His	Tyr	Ala	Thr	Met	Ala	
865					870					875					880	
Arg	Ser	Ala	Val	Arg	Pro	Ala	Ser	Leu	Asn	Leu	Asn	Arg	Ser	Arg	Ser	
				885					890					895		
Leu	Ser	Asn	Ser	Asn	Pro	Asp	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Pro	Asp	
			900					905					910			
Asp	Glu	Val	Arg	Ser	Ile	Ile	Gly	Ser	Lys	Gly	Leu	Asp	Arg	Ser	Asn	
		915					920					925				
Ser	Trp	Val	Asn	Thr	Gly	Gly	Pro	Lys	Ala	Ala	Pro	Trp	Gly	Ser	Asn	
	930					935					940					
Pro	Ser	Pro	Ser	Ala	Glu	Ser	Thr	Gln	Ala	Met	Asp	Arg	Ser	Cys	Asn	
945					950					955					960	
Arg	Met	Ser	Ser	His	Thr	Glu	Thr	Ser	Ser	Phe	Leu	Gln	Thr	Leu	Thr	
				965					970					975		
Gly	Arg	Leu	Pro	Thr	Lys	Lys	Leu	Phe	His	Glu	Glu	Leu	Ala	Leu	Gln	
			980					985					990			
Trp	Val	Val	Cys	Ser	Gly	Ser	Val	Arg	Glu	Ser	Ala	Leu	Gln	Gln	Ala	
		995					1000					1005				
Trp	Phe	Phe	Phe	Glu	Leu	Met	Val	Lys	Ser	Met	Val	His	His	Leu	Tyr	
	1010					1015					1020					
Phe	Asn	Asp	Lys	Leu	Glu	Ala	Pro	Arg	Lys	Ser	Arg	Phe	Pro	Glu	Arg	
1025					1030					1035				1040		
Phe	Met	Asp	Asp	Ile	Ala	Ala	Leu	Val	Ser	Thr	Ile	Ala	Ser	Asp	Ile	
				1045					1050					1055		
Val	Ser	Arg	Phe	Gln	Lys	Asp	Thr	Glu	Met	Val	Glu	Arg	Leu	Asn	Thr	
			1060					1065					1070			

Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
 1075 1080 1085
 Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
 1090 1095 1100
 Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
 1105 1110 1115 1120
 Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
 1125 1130 1135
 Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser
 1140 1145 1150
 Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
 1155 1160 1165
 Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
 1170 1175 1180
 Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
 1185 1190 1195 1200
 Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
 1205 1210 1215
 His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
 1220 1225 1230
 Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
 1235 1240 1245
 Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
 1250 1255 1260
 Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
 1265 1270 1275 1280
 Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
 1285 1290 1295
 Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
 1300 1305 1310
 Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
 1315 1320 1325
 Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
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 Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390

Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660
 Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710

Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala
 1985 1990 1995 2000
 Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
 2005 2010 2015
 Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
 2020 2025 2030

Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His
 2035 2040 2045
 Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp
 2050 2055 2060
 Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr
 2065 2070 2075 2080
 Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro
 2085 2090

 <210> 102
 <211> 1980
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human CLASP-2

 <400> 102
 Met Leu Leu Phe Pro Tyr Asp Asp Phe Gln Thr Ala Ile Leu Arg Arg
 1 5 10 15
 Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu
 20 25 30
 Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
 35 40 45
 Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
 50 55 60
 Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
 65 70 75 80
 Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
 85 90 95
 Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
 100 105 110
 Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
 115 120 125
 Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
 130 135 140
 Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
 145 150 155 160
 Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
 165 170 175
 Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
 180 185 190
 Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
 195 200 205

Gln	Leu	Asn	Phe	Glu	Ala	Ala	Met	Gln	Glu	Lys	Arg	Asn	Gly	Asp	Ser		
210						215					220						
His	Glu	Asp	Asp	Glu	Gln	Ser	Lys	Leu	Glu	Gly	Ser	Gly	Ser	Gly	Leu		
225					230					235					240		
Asp	Ser	Tyr	Leu	Pro	Glu	Leu	Ala	Lys	Ser	Ala	Arg	Glu	Ala	Glu	Ile		
				245					250					255			
Lys	Leu	Lys	Ser	Glu	Ser	Arg	Val	Lys	Leu	Phe	Tyr	Leu	Asp	Pro	Asp		
			260					265					270				
Ala	Gln	Lys	Leu	Asp	Phe	Ser	Ser	Ala	Glu	Pro	Glu	Val	Lys	Ser	Phe		
		275					280					285					
Glu	Glu	Lys	Phe	Gly	Lys	Arg	Ile	Leu	Val	Lys	Cys	Asn	Asp	Leu	Ser		
	290					295					300						
Phe	Asn	Leu	Gln	Cys	Cys	Val	Ala	Glu	Asn	Glu	Glu	Gly	Pro	Thr	Thr		
305					310					315					320		
Asn	Val	Glu	Pro	Phe	Phe	Val	Thr	Leu	Ser	Leu	Phe	Asp	Ile	Lys	Tyr		
				325					330					335			
Asn	Arg	Lys	Ile	Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Phe	Ser		
			340					345					350				
Val	Arg	Gln	Met	Leu	Ala	Thr	Thr	Ser	Pro	Ala	Leu	Met	Asn	Gly	Ser		
		355					360					365					
Gly	Gln	Ser	Pro	Ser	Val	Leu	Lys	Gly	Ile	Leu	His	Glu	Ala	Ala	Met		
	370					375					380						
Gln	Tyr	Pro	Lys	Gln	Gly	Ile	Phe	Ser	Val	Thr	Cys	Pro	His	Pro	Asp		
385					390					395					400		
Ile	Phe	Leu	Val	Ala	Arg	Ile	Glu	Lys	Val	Leu	Gln	Gly	Ser	Ile	Thr		
				405					410					415			
His	Cys	Ala	Glu	Pro	Tyr	Met	Lys	Ser	Ser	Asp	Ser	Ser	Lys	Val	Ala		
			420					425					430				
Gln	Lys	Val	Leu	Lys	Asn	Ala	Lys	Gln	Ala	Cys	Gln	Arg	Leu	Gly	Gln		
		435					440					445					
Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	Ala	Arg	Thr	Leu	Phe	Lys	Asp	Ala		
	450					455					460						
Ser	Gly	Asn	Leu	Asp	Lys	Asn	Ala	Arg	Phe	Ser	Ala	Ile	Tyr	Arg	Gln		
465					470					475				480			
Asp	Ser	Asn	Lys	Leu	Ser	Asn	Asp	Asp	Met	Leu	Lys	Leu	Leu	Ala	Asp		
				485				490						495			
Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly	Asn		
			500					505					510				
Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr	Val		
	515						520					525					

Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr
530						535					540				
Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His
545					550					555					560
Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys
				565					570					575	
Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile
			580					585					590		
Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro
		595					600					605			
Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser
	610					615					620				
Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp
625					630					635					640
Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu
				645					650					655	
Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser
			660					665					670		
Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu
		675					680					685			
Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro
	690					695					700				
Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly
705					710					715					720
Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys
				725					730					735	
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln
			740					745					750		
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser
		755					760					765			
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu
	770					775					780				
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu
785					790					795					800
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala
				805					810					815	
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu
			820					825					830		
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys
		835					840					845			

Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
 1170 1175 1180
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
 1185 1190 1195 1200
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
 1205 1210 1215
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
 1220 1225 1230
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340
 Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
 1345 1350 1355 1360
 Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
 1365 1370 1375
 Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
 1380 1385 1390
 Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
 1395 1400 1405
 Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
 1410 1415 1420
 Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
 1425 1430 1435 1440
 Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
 1445 1450 1455
 Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
 1460 1465 1470
 Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
 1475 1480 1485

Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
 1490 1495 1500
 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
 1505 1510 1515 1520
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1525 1530 1535
 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1540 1545 1550
 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
 1555 1560 1565
 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
 1570 1575 1580
 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
 1585 1590 1595 1600
 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 1605 1610 1615
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 1620 1625 1630
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 1635 1640 1645
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
 1650 1655 1660
 Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
 1665 1670 1675 1680
 Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695
 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710
 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn
 1715 1720 1725
 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
 1730 1735 1740
 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
 1745 1750 1755 1760
 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775
 Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790
 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805

Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935
 Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
 1940 1945 1950
 Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
 1955 1960 1965
 Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
 1970 1975 1980

<210> 103
 <211> 2045
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-7

<400> 103
 Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile Asn Arg Thr
 1 5 10 15
 Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg Ser Gly Ser
 20 25 30
 Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr
 35 40 45
 Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
 50 55 60
 Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
 65 70 75 80
 Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
 85 90 95

Pro	Gly	Ile	Pro	Lys	Asp	Glu	Lys	Leu	Asp	Ala	Gln	Val	Arg	Ala	Ala	
			100					105					110			
Val	Glu	Met	Tyr	Ile	Glu	Asp	Trp	Val	Ile	Val	His	Arg	Arg	Tyr	Gln	
		115					120					125				
Tyr	Leu	Ser	Ala	Ala	Tyr	Ser	Pro	Val	Thr	Thr	Asp	Thr	Gln	Arg	Glu	
	130					135					140					
Arg	Gln	Lys	Gly	Leu	Pro	Arg	Gln	Val	Phe	Glu	Gln	Asp	Ala	Ser	Gly	
145					150				155						160	
Asp	Glu	Arg	Ser	Gly	Pro	Glu	Asp	Ser	Asn	Asp	Ser	Arg	Arg	Gly	Ser	
				165					170					175		
Gly	Ser	Pro	Glu	Asp	Thr	Pro	Arg	Ser	Ser	Gly	Ala	Ser	Ser	Ile	Phe	
			180					185					190			
Asp	Leu	Arg	Asn	Leu	Ala	Ala	Asp	Ser	Leu	Leu	Pro	Ser	Leu	Leu	Glu	
		195					200					205				
Arg	Ala	Ala	Pro	Glu	Asp	Val	Asp	Arg	Arg	Asn	Glu	Thr	Leu	Arg	Arg	
	210					215					220					
Gln	His	Arg	Pro	Pro	Ala	Leu	Leu	Thr	Leu	Tyr	Pro	Ala	Pro	Asp	Glu	
225					230					235					240	
Asp	Glu	Ala	Val	Glu	Arg	Cys	Ser	Arg	Pro	Glu	Pro	Pro	Arg	Glu	His	
				245				250					255			
Phe	Gly	Gln	Arg	Ile	Leu	Val	Lys	Cys	Leu	Ser	Leu	Lys	Phe	Glu	Ile	
			260					265					270			
Glu	Ile	Glu	Pro	Ile	Phe	Gly	Ile	Leu	Ala	Leu	Tyr	Asp	Val	Arg	Glu	
		275					280					285				
Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu	Asn	Ser	Asp	Ser	
	290					295					300					
Met	Lys	Gly	Leu	Leu	Arg	Ala	His	Gly	Thr	His	Pro	Ala	Ile	Ser	Thr	
305					310					315					320	
Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Val	Thr	Tyr	Pro	Ser	Pro	Asp	Ile	
				325					330					335		
Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	Gly	Asp	Ile	Ser	
			340					345					350			
Glu	Cys	Cys	Glu	Pro	Tyr	Met	Val	Leu	Lys	Glu	Val	Asp	Thr	Ala	Lys	
		355					360					365				
Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Arg	Leu	Ala	Ala	Glu	Gln	Phe	Cys	
	370					375					380					
Thr	Arg	Leu	Gly	Arg	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Thr	Ala	Val	His	
385					390					395					400	
Leu	Ala	Asn	Ile	Val	Ser	Ser	Ala	Gly	Gln	Leu	Asp	Arg	Asp	Ser	Asp	
				405					410					415		

Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
 420 425 430
 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
 435 440 445
 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
 450 455 460
 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
 465 470 475 480
 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu
 485 490 495
 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605
 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
 610 615 620
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
 625 630 635 640
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
 660 665 670
 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
 725 730 735

Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
 740 745 750
 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
 785 790 795 800
 Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
 805 810 815
 Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
 820 825 830
 Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
 835 840 845
 Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
 850 855 860
 Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
 865 870 875 880
 Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
 885 890 895
 Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
 900 905 910
 Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu
 915 920 925
 Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
 930 935 940
 His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
 945 950 955 960
 Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
 965 970 975
 Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
 980 985 990
 Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
 995 1000 1005
 Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
 1010 1015 1020
 Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
 1025 1030 1035 1040
 Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
 1045 1050 1055

Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
 1060 1065 1070
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
 1075 1080 1085
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
 1090 1095 1100
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
 1105 1110 1115 1120
 Leu Gln Glu Asp Gln Asp Val Arg His Leu Ala Leu Ala Val Leu Lys
 1125 1130 1135
 Asn Leu Met Ala Lys His Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg
 1140 1145 1150
 Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu
 1155 1160 1165
 Leu Asp Asn Met Pro Arg Ile Arg Leu His Asp Phe Ala Glu Gly Pro
 1170 1175 1180
 Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr Glu Gly
 1185 1190 1195 1200
 Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met Ala Ile
 1205 1210 1215
 Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser Gln Gly
 1220 1225 1230
 Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu Ser Ser
 1235 1240 1245
 Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr Glu Pro
 1250 1255 1260
 Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln Leu Gly
 1265 1270 1275 1280
 Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu Tyr Lys
 1285 1290 1295
 Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys Lys Ser
 1300 1305 1310
 Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr Ile Gly
 1315 1320 1325
 Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro Phe Gly
 1330 1335 1340
 Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp Lys Gln
 1345 1350 1355 1360
 Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His Glu Ala
 1365 1370 1375

Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val Leu Asp
 1380 1385 1390
 Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala Arg Glu
 1395 1400 1405
 Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu Gly Ser
 1410 1415 1420
 Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln Arg Ala
 1425 1430 1435 1440
 Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr Glu Leu
 1445 1450 1455
 Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser Arg Ile
 1460 1465 1470
 Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu Met Arg
 1475 1480 1485
 Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met Gln Val
 1490 1495 1500
 Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe Ser Glu
 1505 1510 1515 1520
 Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu
 1525 1530 1535
 Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln Asp Leu
 1540 1545 1550
 Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu
 1555 1560 1565
 His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala
 1570 1575 1580
 Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn
 1585 1590 1595 1600
 Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln
 1605 1610 1615
 Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu
 1620 1625 1630
 Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile
 1635 1640 1645
 Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser
 1650 1655 1660
 Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly
 1665 1670 1675 1680
 Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly
 1685 1690 1695

Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu
 1700 1705 1710
 Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu
 1715 1720 1725
 Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg
 1730 1735 1740
 Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly
 1745 1750 1755 1760
 Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys
 1765 1770 1775
 Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe
 1780 1785 1790
 Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys
 1795 1800 1805
 Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu
 1810 1815 1820
 Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp
 1825 1830 1835 1840
 Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe Thr Pro
 1845 1850 1855
 Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg Lys Thr
 1860 1865 1870
 Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg
 1875 1880 1885
 Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile
 1890 1895 1900
 Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln
 1905 1910 1915 1920
 Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val
 1925 1930 1935
 Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu
 1940 1945 1950
 Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu
 1955 1960 1965
 Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala Leu Arg
 1970 1975 1980
 Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu
 1985 1990 1995 2000
 Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu
 2005 2010 2015

Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg
2020 2025 2030

Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
2035 2040 2045

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20 25 30
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35 40 45
Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
50 55 60
Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
65 70 75 80
Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
85 90 95
Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
100 105 110
Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
115 120 125
Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
130 135 140
Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
145 150 155 160
Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val
165 170 175
Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn
180 185 190
Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr
195 200 205
Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys
210 215 220
Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
225 230 235 240

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Glu	Thr	Glu	Asp	Thr	Val	Lys	Thr	Thr	Arg	Asn	Met	Glu	Arg	Leu	Asn	
			340					345					350			
Leu	Phe	Ser	Leu	Asp	Pro	Asp	Ile	Asp	Thr	Leu	Lys	Leu	Gln	Lys	Lys	
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Asp	Leu	Leu	Glu	Pro	Glu	Ser	Val	Ile	Lys	Pro	Phe	Glu	Glu	Lys	Ala	
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Ala	Lys	Arg	Ile	Met	Ile	Ile	Cys	Lys	Ala	Leu	Asn	Ser	Asn	Leu	Gln	
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Phe	Phe	Val	Ser	Val	Ala	Leu	Tyr	Asp	Leu	Arg	Asp	Ser	Arg	Lys	Ile	
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Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Ala	Ala	Val	Arg	Gln	Met	
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Leu	Leu	Gly	Ala	Ser	Val	Ala	Leu	Glu	Asn	Gly	Asn	Ile	Asp	Thr	Ile	
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Thr	Pro	Arg	Gln	Ser	Glu	Glu	Pro	His	Ile	Lys	Gly	Leu	Pro	Glu	Glu	
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Trp	Leu	Lys	Phe	Pro	Lys	Gln	Ala	Val	Phe	Ser	Val	Ser	Asn	Pro	His	
				485					490					495		
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Ile	Ala	Ser	Gly	Ala	Glu	Pro	Tyr	Ile	Lys	Asn	Pro	Asp	Ser	Asn	Lys	
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Tyr	Ala	Gln	Lys	Ile	Leu	Lys	Ser	Asn	Arg	Gln	Phe	Cys	Ser	Lys	Leu	
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Ser	Asp	Tyr	Arg	Arg	Ala	Asp	Arg	Ile	Ser	Lys	Met	Gln	Thr	Ile	Pro		
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Gly	Ser	Leu	Asp	Ile	Ala	Val	Asp	Asn	Val	Pro	Leu	Glu	His	Pro	Asn		
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Cys	Val	Thr	Ser	Ser	Phe	Ile	Pro	Val	Lys	Pro	Phe	Asn	Met	Met	Ala		
625					630					635					640		
Gln	Thr	Glu	Pro	Thr	Val	Glu	Val	Glu	Glu	Phe	Val	Tyr	Asp	Ser	Thr		
				645				650						655			
Lys	Tyr	Cys	Arg	Pro	Tyr	Arg	Val	Tyr	Lys	Asn	Gln	Ile	Tyr	Ile	Tyr		
			660					665					670				
Pro	Lys	His	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Cys	Phe	Asn	Lys	Ala	Arg		
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Asn	Ile	Thr	Val	Cys	Ile	Glu	Phe	Lys	Asn	Ser	Asp	Glu	Glu	Ser	Ala		
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Lys	Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Lys	Pro	Glu	Gly	Pro	Leu	Phe	Thr		
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Ser	Ala	Ala	Tyr	Thr	Ala	Val	Leu	His	His	Ser	Gln	Asn	Pro	Asp	Phe		
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Ser	Asp	Glu	Val	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His		
			740					745					750				
His	Ile	Leu	Phe	Ser	Phe	Tyr	His	Val	Thr	Cys	Asp	Ile	Asn	Ala	Lys		
		755					760					765					
Ala	Asn	Ala	Lys	Lys	Lys	Glu	Ala	Leu	Glu	Thr	Ser	Val	Gly	Tyr	Ala		
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Trp	Leu	Pro	Leu	Met	Lys	His	Asp	Gln	Ile	Ala	Ser	Gln	Glu	Tyr	Asn		
785					790					795					800		
Ile	Pro	Ile	Ala	Thr	Ser	Leu	Pro	Pro	Asn	Tyr	Leu	Ser	Phe	Gln	Asp		
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Ser	Ala	Ser	Gly	Lys	His	Gly	Gly	Ser	Asp	Ile	Lys	Trp	Val	Asp	Gly		
			820					825					830				
Gly	Lys	Pro	Leu	Phe	Lys	Val	Ser	Thr	Phe	Val	Val	Ser	Thr	Val	Asn		
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	850					855					860						
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865					870					875					880		

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 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
 900 905 910
 Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
 915 920 925
 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
 930 935 940
 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
 945 950 955 960
 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
 965 970 975
 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
 980 985 990
 Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
 995 1000 1005
 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
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 1125 1130 1135
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 Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp
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 Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His
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 1250 1255 1260
 Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser
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 Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala
 1300 1305 1310
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 1315 1320 1325
 Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr
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 Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser
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 1365 1370 1375
 Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val
 1380 1385 1390
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 Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His
 1410 1415 1420
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 1425 1430 1435 1440
 Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
 1445 1450 1455
 Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr
 1460 1465 1470
 Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val
 1475 1480 1485
 Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys
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Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu
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 Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe
 1570 1575 1580
 Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser
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 Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val
 1635 1640 1645
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
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 Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
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 Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
 1685 1690 1695
 Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
 1700 1705 1710
 Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
 1715 1720 1725
 Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
 1730 1735 1740
 Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
 1745 1750 1755 1760
 Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
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 Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
 1780 1785 1790
 Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
 1795 1800 1805
 Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
 1810 1815 1820
 Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
 1825 1830 1835 1840

Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
 1845 1850 1855
 Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
 1860 1865 1870
 Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys
 1875 1880 1885
 Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
 1890 1895 1900
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
 1905 1910 1915 1920
 Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
 1925 1930 1935
 Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
 1940 1945 1950
 Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
 1955 1960 1965
 Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
 1970 1975 1980
 Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
 1985 1990 1995 2000
 His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
 2005 2010 2015
 Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
 2020 2025 2030
 Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
 2035 2040 2045
 Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
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 Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
 2065 2070 2075 2080
 Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
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 Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
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 Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
 2115 2120 2125
 Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
 2130 2135 2140
 Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
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Ser Ala Glu Val
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(ITAM) motif 2

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<212> PRT
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<220>
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immunoreceptor tyrosine-based activation motif
(ITAM) motif 3

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<211> 9
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conserved non-tyrosine containing region from
motif E

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Ile or Leu

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Asp, Glu or Gln

<220>
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<220>
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Met, Ile, Leu or Val

<400> 131
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<210> 132
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motif F

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Gln or Asn

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primer HC4AS3'

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21

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Anal
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<210> 148
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used for human CLASP-3 5' RACE

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28



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Dossier: 09737246

Legal Date: 10-04-2001

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Total number of pages: 7

Remarks:

Order of re-scan issued on